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H. pylori antigens

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The present invention relates to isolated nucleic acid molecules, which encode antigens for *Helicobacter pylori,* which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Helicobacter pylori.*

Helicobacter pylori is a Gram-negative, microaerobic, spiral and flagellated bacterium representing the most prevalent human pathogen with nearly half the globe's population infected. Infection most likely occurs in early childhood (< age 10) in most cases and the pathogen specifically colonizes the stomach where it becomes a resident. Colonization lasts for years or even decades but it can persist for life, yet about 70-80 % of colonized individuals remain asymptomatic and never develop disease. It is now clear that the prolonged interaction of *H. pylori* with gastric epithelia is a complex and dynamic process, which leads to chronic acute inflammation of the gastric mucosa and to the development of peptic ulcer disease in 10-20 % of the cases. Nearly all duodenal ulcers are caused by *H. pylori* and, in the stomach ulcers can develop into gastric adenocarcinoma with a frequency of 0,1-4 %. The significance of this number is that gastric cancer is the second most common fatal malignancy after lung cancer and within twenty years, it is predicted to be the 8th leading cause of death of any origin worldwide. *H. pylori* infection is also associated with about 90 % of mucosa-associated lymphoid tissue lymphomas (MALT). Patients with *H. pylori* infection develop high titers of primarily IgG and IgA antibodies but their role in the immune response against the bacterium is not known. Presence of the bacteria within the mucosal epithelium is associated with massive neutrophil infiltration. Considerable evidence exists demonstrating that the *H. pylori* -induced Th1-biased $CD4^+$ T cell response with prominent IFN-γ production might be a strong contributing factor in the outcome of the local immune reaction linked to tissue damage.

H. pylori is inherently equipped with an array of extremely potent factors and mechanisms that enable the pathogen to uniquely adapt to the gastric mucosal environment leading to survival and long-term colonization in humans. However, the known virulence factors are only associated with increased risk of disease and are not absolute. Perhaps the most obvious system what *H. pylori* developed is its powerful urease enzyme, which by converting urea into ammonia and carbon dioxide allows survival under acidic conditions. Expression of the cytoplasmic apoenzyme is constitutive and its abundance can be as high as 15 % of total *H. pylori* protein. The activity of the enzyme is increased in low pH and the conductance of the inner membrane is also increased for urea under low pH conditions. The produced NH_3 diffuses to the periplasm protecting thereby the bacterium against the extremely acidic environment {Prinz, C. et al., 2003}. The vacuolating cytotoxin product of the *vacA* gene of *H. pylori* induces vacuole formation and, thus, perturbation of structure and function in epithelial cells. The *vacA* gene is present in all strains but its expression varies. It is now known that VacA acts through a Z-type protein tyrosine phosphatase receptor by increasing its tyrosine phosphorylation activity on the G-protein coupled receptor kinase-interactor 1, leading to marked detachment of gastric epithelial cells from their base membrane, a possible mechanism behind *H. pylori* -induced epithelial cell demise and consequent peptic ulcer formation {Fujikawa, A. et al., 2003}. A major virulence-associated genetic element in *H. pylori* is the 40 Kbp pathogenicity island, Cag (cytotoxin associated gene) PAI, contained in the majority of strains. The PAI harbors about 30 genes and one gene product, CagA was originally identified in serological studies as an important determinant of disease outcome in *H. pylori* infected individuals. The Cag PAI contains genes that have close sequence similarities to a type IV secretion system, known to provide a mechanism for direct transfer of bacterial effector proteins into eukaryotic host cells. Not surprising therefore that the CagA protein has been demonstrated as the effector protein that translocates from adherent *H. pylori* into epithelial cells *in vitro*. The subsequently phosphorylated CagA rearranges the host cytoskeleton, which then leads to pedestal formation adjacent to the bacteria {Bjorkholm, B. et al., 2003}. Although, it is present in strains expressing VacA, the *cagA* gene is not linked chromosomally to *vacA*. Strains with the *cagA* PAI and the *vacA* genotype (type I strains) are associated with higher frequency with patients suffering from duodenal ulcer, atrophic gastritis and gastric carcinoma compared with those lacking CagA and VacA (type II strains) {Censini, S. et al., 1996}. Human populations in distinct geographical regions can be differentiated based on genotypic variations located to the right end of the *cag* PAI {Kersulyte, D. et al., 2000}.

Attachment of *H. pylori* to gastric epithelium is promoted by a number of factors. The Hpa hemagglutinin binds to sialic acid components of erythrocytes while the *babA2*-encoded BabA adhesion binds to the histo-blood group antigen Lewis^{b}, present on gastric epithelial cells. *babA2*-positive strains are more frequently isolated from patients with peptic ulcer disease and gastric carcinoma than type 1 strains and, when compared to type 1 strains lacking *babA2*, type 1 isolates that also harbor the *babA2* gene are more prevalent in patients with atrophic gastritis and intestinal metaplasia. The SabA adhesion protein is shown to associate with a glycoconjugate on the onco-fetal surface antigen sialyl-Le^{x} that is expressed on immature cells of the developing fetal gastric epithelium as well as on rapidly proliferating undifferentiated cells of cancerous and precancerous lesions {Dubreuil, J. et al., 2002}.

Another potent virulence-associated mechanism evolved in *H. pylori* is its natural competence for transformation together with the pathogen's highest rate of recombination of any known bacterial species. This mechanism makes *H. pylori* capable of acquiring new genetic material via horizontal gene transfer, a common phenomenon during colonization of an individual and this can result in the generation of novel pathogen subtypes (quasispecies) that exhibit profound changes in virulence markers, such as the *cag* PAI {Loughlin, M. et al., 2003}. Such extreme genetic variability, with any given isolate easily distinguishable from most others by DNA fingerprinting, has also been proposed to account for the expression diversity of many cell surface associated or secreted proteins {Ferrero, R. et al., 2001}. Although, it is not yet clear why only a relatively small portion of the infected population develop clinically manifest disease, the above mentioned pathogen-related factors together with emerging host-specific characteristics, such as IL-1β promoter allele polymorphism, are likely contribute to the complex mechanisms that lie behind *H. pylori* pathogenicity {Blaser, M., 2000}.

Today, patients diagnosed with *H. pylori* infection are treated with a combination of one or two antibiotics and a proton pump inhibitor or bismuth. There are a number of standard combinations but re-infection (most likely from parts of the stomach where eradication did not happen) can occur. Current combinational treatment regimes reach 80-90 % eradication rates in most cases but since *H. pylori* strains are emerging with resistance to one or more of the antibiotics that currently comprise any of the treatment combinations, development of new strategies is urgently needed for an effective treatment to prevent or ameliorate *H.pylori* infections. A vaccine could not only prevent infections by Helicobacter, but more specifically prevent or ameliorate colonization of host tissues, thereby reducing the incidence of gastric atrophy, peptic ulcer disease and gastric cancer. Elimination of severe chronic conditions would be a direct consequence of reducing the incidence of acute infection and carriage of the organism.

A vaccine can contain a whole variety of different antigens. Examples of antigens are whole-killed or attenuated organisms, subfractions of these organisms/tissues, proteins, or, in their most simple form, peptides. Antigens can also be recognized by the immune system in form of glycosylated proteins or peptides and may also be or contain polysaccharides or lipids. Short peptides can be used since for example cytotoxic T-cells (CTL) recognize antigens in form of short usually 8-11 amino acids long peptides in conjunction with major histocompatibility complex (MHC). B-cells can recognize linear epitopes as short as 4-5 amino acids, as well as three-dimensional structures (conformational epitopes). In order to obtain sustained, antigen-specific immune responses, adjuvants need to trigger immune cascades that involve all cells of the immune system necessary. Primarily, adjuvants are acting, but are not restricted in their mode of action, on so-called antigen presenting cells (APCs). These cells usually first encounter the antigen(s) followed by presentation of processed or unmodified antigen to immune effector cells. Intermediate cell types may also be involved. Only effector cells with the appropriate specificity are activated in a productive immune response. The adjuvant may also locally retain antigens and co-injected other factors. In addition the adjuvant may act as a chemoattractant for other immune cells or may act locally and/or systemically as a stimulating agent for the immune system.

Attempts to develop a Helicobacter vaccine have focused mainly on whole-cell and attenuated or subunit

vaccine approaches. The initial "proof of principle" studies to generate an *H. pylori* vaccine were performed using inactivated whole-cell preparations and cholera toxin as a mucosal adjuvant. Although, such vaccines were highly effective in inducing protective immunity against gastric infection in mice, their safety and licensing as well as difficulties in producing *H. pylori* preparations *in vitro* in large scale eliminated them from human trials {Ferrero, R. et al., 2001}; {Sutton, P., 2001}. For second generation subunit vaccines, candidate antigens were identified by empirical approaches. The selection criteria for these antigens were linked to known or suspected roles of the proteins in bacterial virulence. Such candidates include the urease holenzyme and its subunits, UreA and UreB, heat shock protein homologues of the chaperonins GroEL and GroES, the VacA cytotoxin and catalase (KatA) ({Prinz, C. et al., 2003}; {Svennerholm, A., 2003} and references therein). Another set of candidate proteins were identified in subsequent studies on the basis of their immunoreactivity in *in vitro* assays. *H. pylori* genomic expression libraries were screened with antibodies from mice that had been immunized with *H. pylori* whole cell sonicates or outer membrane vesicles in the presence of cholera toxin. Antigenic proteins were purified from selected *E. coli* clones and their identity determined by N-terminal sequencing. Among known antigens, such as UreA, UreB, the GroEL homologue and Lpp20 lipoprotein, four previously uncharacterized proteins were also identified. One had homology to L7/L12 ribosomal proteins and the rest were of unknown function. A similar screening strategy combined with a chimeric fusion technique confirmed the Lpp20 protein as a vaccine candidate antigen {Oliaro, J. et al., 2000}. There are other proteins under consideration for vaccine development that are based on recent identifications employing multiparameter selection criteria. These include an Hpa homologue (HP0410) and a novel protein of unknown function (HP0231), both with high protective efficacy {Sabarth, N. et al., 2002}. Despite the benefits of both prophylactic and therapeutic vaccination in animals as demonstrated in several studies, bacterial eradication (sterilizing immunity) has not been described in humans.

Since the above mentioned identification methods are either empirical or limited to a specific selection criterion, there is a demand to identify additional relevant antigens of *H. pylori* using an efficient and comprehensive identification and validation technology.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic potency and genetic background, *Helicobacter pylori* is distinctive from Staphylococcus strains. Importantly, the selection of sera for the identification of antigens from *H. pylori* is different from that applied to the *S. aureus* screens.

Three major types of human sera were collected for this purpose. First, healthy adults below <45 years of age were tested for *H. pylori*-specific IgG and IgA serum antibody levels by ELISA using total bacterial lysate and culture supernatant proteins. High titer individuals were interviewed and seleted based on the absence of medical history, symptoms or complains related to *H. pylori* diseases. Based on correlative data, protective (colonization neutralizing) antibodies are likely to be present in exposed individuals who are not carriers of *H. pylori* or not susceptible to disease casued by *H. pylori*. High titer sera from symptom-free healthy adults were included in the genomic based antigen identification. This approach for selection of human sera is basically very different from that used for *S. aureus*, where carriage or noncarriage state cannot be associated with antibody levels.
Second, serum samples from patients with gastric cancer were characterized for anti-*H.* pylori antibody titers using ELISA and high titer sera were selected for the screens. The third group of serum samples was obtained from individuals with duodenal ulcer and high titer sera determined by ELISA were selected for the screens.

The genomes of the two bacterial species *H. pylori* and *S. aureus* by itself show a number of important differences. The genome of *H. pylori* contains approximately 1.65 Mb sequence information, while *S. aureus* harbours about 2.85 Mb. They have an average GC content of 39 and 33%, respectively. In

addition, the two bacterial species require different growth conditions and media for propagation. While *H. pylori* is a strictly human pathogen, *S. aureus* can also be found infecting a range of warm-blooded animals. A list of the most important diseases, which can be inflicted by the two pathogens, is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impetigo, folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumonia, osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *H. pylori* causes likely community aquired gastro-intestinal infections: self limiting traveler's diarrhea, corpus predominant or pangastritis, peptic ulcer disease (stomach and duodenum), gastric cancer (adenocarcinoma), chronic atrophic gastritis (CAG) and MALT (mucosa-associated lymphoid tissue, non-Hodgkin's type B cell lymphoma).

The problem underlying the present invention was to provide means for the development of medicaments such as vaccines against *H. pylori* infection. Particularly, the problem was to provide an efficient, relevant and comprehensive set of nucleic acid molecules or antigens from *H. pylori* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:

a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No** 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178.
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least 80%, preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from **Seq ID No** 8-10, 13-15, 17-18, 24, 27, 32, 39-40, 45-47, 56, 59, 62, 69-70, 73, 77, 79, 82, 85-86, 88, 90, 103, 109-110, 114, 121,
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

According to another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule selected from **Seq ID No** 5, 7, 30-31, 53, 60, 66, 76, 83, 87, 92, 99, 120,
b) a nucleic acid molecule which is complementary to the nucleic acid of a),
c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a *H. pylori* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the aspects of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 181-182, 194, 197-199, 206-207, 211-216, 219-220, 222, 226-230, 233, 235-236, 239, 241, 243, 245-246, 250, 252-253, 259, 262, 269, 272, 274-275, 279, 283-286, 290, 293-295, 297, 301-356.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 186-188, 191-193, 195-196, 202, 205, 210, 217-218, 223-225, 234, 237, 240, 247-248, 251, 255, 257, 260, 263-264, 266, 268, 281, 287-288, 292, 299.

In a further preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 183, 185, 208-209, 231, 238, 244, 254, 261, 265, 270, 277, 298.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1, especially peptides comprising amino acids 63-91, 95-101, 110-116, 134-148, 150-156, 158-164, 188-193, 197-209, 226-241, 247-254, 291-297, 312-319, 338-346, 351-358, 366-378, 404-410, 420-438, 448-454, 465-473, 482-488, 490-498, 503-510, 512-519, 531-543, 547-554, 568-575, 589-604, 610-631 and 239-308 of Seq ID No 179; 16-29, 35-47, 50-68, 70-79, 91-101, 143-149, 158-163, 185-191, 196-206, 215-224, 230-237, 244-251, 258-278, 290-311, 319-325, 338-351, 365-385, 396-429, 445-454, 458-466, 491-499, 501-521, 17-79 and 218-233 of Seq ID No 180; 4-10, 16-41, 46-66, 77-84, 91-97, 102-118, 125-144, 187-200, 202-214, 245-253, 255-261, 286-295, 300-330, 335-342, 350-361, 363-381, 385-392, 396-416, 435-450 and 460-470 of Seq ID No 181; 11-19, 27-48, 52-59, 77-82, 84-107, 118-125, 127-154, 178-183, 192-209, 215-221, 286-295, 302-313, 350-357, 402-415, 417-431, 453-463, 465-493 and 313-331 of Seq ID No 182; 19-26, 30-43, 47-55, 63-68, 72-80, 97-104, 107-119, 129-146, 160-175, 194-216, 231-251, 254-260 and 26-43 of Seq ID No 183; 7-13, 29-37, 65-81, 110-120, 123-131, 135-152, 230-249, 254-260, 284-290, 292-299, 317-326, 329-336, 403-444, 452-458, 466-477, 490-498, 510-519, 541-550, 557-566 and 533-567 of Seq ID No 184; 5-47, 71-77, 79-86, 89-95, 120-126, 137-144, 176-181, 184-196, 202-208, 211-232, 236-282, 301-313, 317-325, 341-347, 353-384, 394-400, 412-433, 436-443 and 59-75 of Seq ID No 185; 4-18, 22-38, 59-69, 106-112, 116-130, 138-149, 156-170, 175-197, 200-214, 216-223, 233-244, 255-261, 266-276, 279-286, 325-333, 342-348, 366-399, 402-420, 429-441, 1-104 and 130-147 of Seq ID No 186; 50-58, 69-95, 97-113, 131-136, 157-163, 170-175, 188-212, 220-226, 254-259, 265-277, 283-289, 297-308, 311-318, 347-358, 360-369, 378-401, 416-421, 440-450, 454-462, 470-476, 493-502, 506-514, 536-567, 585-590, 598-607, 613-618, 653-659 and 35-46 of Seq ID No 187; 16-29, 32-60, 65-87, 89-123, 128-134, 137-158, 162-173, 178-196, 210-216, 218-228 and 206-225 of Seq ID No 188; 10-20, 26-35, 51-64, 86-91, 94-100, 113-122, 154-160, 185-191, 193-

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The present invention also provides a process for producing a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKLSKLK, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *H. pylori* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to the present invention.

Moreover, the present invention provids a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal,
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation of a medicament for treating or preventing *H. pylori* infections.

According to another aspect the present invention provides an antagonist, which binds to a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment thereof according to the present invention may be identified by a method comprising the following steps:

a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to the present invention with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention to its interaction partner may be identified by a method comprising the following steps:

a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to the present invention,
b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to the present invention,
c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
d) providing a candidate antagonist,
e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex ,
f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *H. pylori* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *H. pylori* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *H. pylori*. Thus, the present invention fulfils a widely felt demand for *H. pylori* antigens, vaccines, diagnostics and products useful in procedures for preparing antibodies and for identifying compounds effective against *H. pylori* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of *H. pylori*. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of *H. pylori*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction of *H. pylori* proteins or peptides with the antibodies present in human sera. The antibodies produced against *H. pylori* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins as identified by the bacterial surface display expression libraries using pools of pre-selected sera are processed in a second and third round of screening by individual selected or generated sera. Thus the present invention supplies an efficient, relevant, comprehensive set of *H. pylori* antigens as promising candidates for the development of a pharmaceutical composition, especially a vaccine preventing infection by *H. pylori*.

In the antigen identification program for identifying a comprehensive set of antigens according to the present invention, at least two different bacterial surface expression libraries are screened with several serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). The antibody pools are derived from a serum collection, which has been tested against antigenic compounds of *H. pylori*, such as whole cell extracts and culture supernatant proteins. Preferably, 2 distinct serum collections are used: 1. With very stable antibody repertoire: normal adults, clinically healthy people, who are non-carriers and overcame previous encounters or currently carriers of *H. pylori* without acute disease and symptoms, 2. With antibodies induced acutely by the presence of the pathogenic organism: patients with manifest disease (e.g. *H. pylori* gastritis, peptic ulcer disease or gastric cancer). Sera have to react with multiple *H. pylori*-specific antigens in order to be considered hyperimmune and therefore relevant in the screening method applied for the present invention. The antibodies produced against *H. pylori* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity.

The expression libraries as used in the present invention should allow expression of all potential antigens, e.g. derived from all surface proteins of *H. pylori*. Bacterial surface display libraries will be represented by a recombinant library of a bacterial host displaying a (total) set of expressed peptide sequences of *H. pylori* on a number of selected outer membrane proteins (LamB, FhuA) at the bacterial host membrane {Georgiou, G., 1997}; {Etz, H. et al., 2001}. One of the advantages of using recombinant expression libraries is that the identified hyperimmune serum-reactive antigens may be instantly produced by expression of the coding sequences of the screened and selected clones expressing the hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning steps necessary.

The comprehensive set of antigens identified by the described program according to the present invention is analysed further by additional rounds of screening. Therefore individual antibody preparations or antibodies generated against selected peptides, which were identified as immunogenic are used. According to a preferred embodiment the individual antibody preparations for the second round of screening are derived from patients who have suffered from infection with *H. pylori*, especially from patients who show an antibody titer above a certain minimum level, for example an antibody titer being higher than 80 percentile, preferably higher than 90 percentile, especially higher than 95 percentile of the human (patient or healthy individual) sera tested. Using such high titer individual antibody preparations in the second screening round allows a very selective identification of the hyperimmune serum-reactive antigens and fragments thereof from *H. pylori*.

Following the high throughput screening procedure, the selected antigenic proteins, expressed as recombinant proteins or in vitro translated products, in case it can not be expressed in prokaryotic expression systems, or the identified antigenic peptides (produced synthetically) are tested in a second screening by a series of ELISA and Western blotting assays for the assessment of their immunogenicity with a large human serum collection (> 50 uninfected, > 100 patients sera).

It is important that the individual antibody preparations (which may also be the selected serum) allow a selective identification of the hyperimmune serum-reactive antigens from all the promising candidates from the first round. Therefore, preferably at least 10 individual antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. It is possible to use also less than 10 individual preparations, however, selectivity of the step may not be optimal with a low number of individual antibody preparations. Therefore, recognition of a given hyperimmune serum-reactive antigen (or an antigenic fragment thereof) by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations confers proper selectivity in the identification process. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *H. pylori* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgA titer above 4,000 U, especially above 6,000 U, and/or an IgG titer above 10,000 U, especially above 12,000 U (U = units, calculated from the OD_{405nm} reading at a given dilution) when the whole organism (total lysate or whole cells) is used as antigen in the ELISA.

The antibodies produced against Helicobacter by the human immune system and present in human sera are indicative of the in vivo expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes by antibodies can be based on sequences as short as 4-5 amino acids. It, however, does not necessarily mean that these short peptides are capable of inducing the given antibody in vivo. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce antibodies against the selected proteins in vivo.

The preferred antigens are located on the cell surface or secreted, and are therefore accessible extracellularly. Antibodies against cell wall proteins are expected to serve two purposes: to inhibit adhesion and to promote phagocytosis or complement mediated killing. Antibodies against secreted proteins are beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within Helicobacter species. Bioinformatic analyses (signal sequences, cell wall localisation signals, transmembrane domains) proved to be very useful in assessing cell surface localisation or secretion. The experimental approach includes the isolation of antibodies with the corresponding epitopes and proteins from human serum, and the generation of immune sera in mice against (poly) peptides selected by the bacterial surface display screens. These sera are then used in a third round of screening as reagents in the following assays: cell surface staining of Helicobacter grown under different conditions (FACS, microscopy), determination of neutralizing capacity (toxin, adherence), and promotion of opsonization and phagocytosis (in vitro phagocytosis assay).

For that purpose, bacterial *E. coli* clones are directly injected into mice and immune sera taken and tested in the relevant in vitro assay for functional opsonic or neutralizing antibodies. Alternatively, specific antibodies may be purified from human or mouse sera using peptides or proteins as substrate.

It is not clear as to what extend host defence against *H. pylori* relies on innate or adaptive immunological mechanisms. The mucous membranes and the gastric acidic environment are formidable barriers against invasion by Helicobacter. However, once the mucous membranes are breached the first line of non-adaptive cellular defence begins its co-ordinate action through complement and phagocytes, especially the polymorphonuclear leukocytes (PMNs) as indicated by the massive neutrophil infiltration of the gastric mucosa in response to the presence of *H. pylori*. Attachment of *H. pylori* induces strong pro-inflammatory cytokine release, including TNF-α, IL-1β and IL-8 that can mediate a local chemoattractant effect for immuno-effector cells, such as granulocytes {Prinz, C. et al., 2003}; {Sutton, P., 2001}. These cells can be regarded as the cornerstones in eliminating invading bacteria. As *H. pylori* is thought to be a exclusively extracellular pathogen, the major anti-Helicobacter adaptive response should come from the humoral arm of the immune system, and this seems to be in agreement with the high titers of primarily

IgG and IgA antibodies that develop in patient upon *H. pylori* infection {Prinz, C. et al., 2003}; {Sutton, P., 2001}. The induction of high titer IgG and sectretory IgA type antibody response may reflect the importance of adaptive mechanisms in the immune response against this organism. In principle, the effect of these antibodies is mediated through three major mechanisms: promotion of opsonization, toxin neutralisation, and inhibition of adherence. It is believed that opsonization is especially important, because of its requirement for an effective phagocytosis. For efficient opsonization the microbial surface has to be coated with antibodies and complement factors for recognition by PMNs through receptors for the Fc fragment of IgG molecules or for activated C3b. After opsonization, the bacteria are phagocytosed and killed. Antibodies bound to specific antigens on the cell surface of bacteria serve as ligands for the attachment to PMNs and to promote phagocytosis. The very same antibodies bound to the adhesins and other cell surface proteins are expected to neutralize adhesion and prevent colonization.

Inducing high affinity antibodies of the opsonic and neutralizing type by vaccination helps the innate immune system to eliminate bacteria and toxins. This makes the method according to the present invention an optimal tool for the identification of *H. pylori* antigenic proteins. The selection of antigens as provided by the present invention is thus well suited to identify those that will lead to protection against infection in an animal model or in humans.

However, there is compelling evidence indicating that antibodies are not required for immunisation-induced effective immunity against gastric helicobacters. Indeed, *in vitro* studies have demonstrated that diminutive fraction of the colonizing *H. pylori* population might enter epithelial cells and this is in good agreement with the fact that *H. pylori* generally induces a predominantly T helper 1 (Th1) type immune response, normally associated with invasive bacteria. Gastric T cells isolated from infected animals and humans produce TNF-α and IFN-γ but not IL-4, typical for a Th1-biased response. This pro-inflammatory Th1 response is clearly not effective against infection {Prinz, C. et al., 2003}; {Sutton, P., 2001}. Current vaccination protocols, such as immunization with recombinant UreB, can drive the immune response to a polarized Th2 phenotype. Studies with knockout mice demonstrated that immunization with urease is possible when the Th2 response is absent. Therefore, vaccine development using new antigens as well as suitable adjuvants that are capable of inducing strong Th1-biased responses may be beneficial in disease protection caused by *H. pylori*.

According to the antigen identification method used herein, the present invention can surprisingly provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens and fragments thereof of *H. pylori*, among other things, as described below. According to one aspect, the invention particularly relates to the nucleotide sequences encoding hyperimmune serum reactive antigens which sequences are set forth in the Sequence listing Seq ID No 1-178, and the corresponding encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in the Sequence Listing Seq ID No 179-356.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhibits 70% identity over their entire length to a nucleotide sequence set forth with Seq ID No 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178. Most highly preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over their entire length to a nucleic acid molecule set forth with Seq ID No 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178. In this regard, nucleic acid molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same are particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98% and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferred, with 100% identity being especially preferred. Moreover, preferred embodiments in this respect are nucleic acids which encode hyperimmune serum reactive antigens or fragments thereof (polypeptides) which retain substantially the same biological function or activity as the mature polypeptide encoded by said nucleic acids set forth in the Seq ID No 3-4, 16, 19-21,

28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178.

Identity, as known in the art and used herein, is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotides or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG program package {Devereux, J. et al., 1984}, BLASTP, BLASTN, and FASTA {Altschul, S. et al., 1990}.

According to another aspect of the invention, nucleic acid molecules are provided which exhibit at least 96% identity to the nucleic acid sequence set forth with **Seq ID No** 8-10, 13-15, 17-18, 24, 27, 32, 39-40, 45-47, 56, 59, 62, 69-70, 73, 77, 79, 82, 85-86, 88, 90, 103, 109-110, 114, 121.

According to a further aspect of the present invention, nucleic acid molecules are provided which are identical to the nucleic acid sequences set forth with **Seq ID No** 5, 7, 30-31, 53, 60, 66, 76, 83, 87, 92, 99, 120.

The nucleic acid molecules according to the present invention can as a second alternative also be a nucleic acid molecule which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C
- Moderate stringency wash in 0.2xSSC, O.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate T_M of 96°C. For 1% mismatch, the T_M is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein is in principle applicable as well.

All nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an

active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Helicobacter pylori strain 26695 and J99* genomes (Nature, 388: 539-547 (1997), 4658-4663; GenBank accession AE000511 and Nature, 397: 176-180 (1999), GenBank accession AE001439) and/or any other published *H. pylori* genome sequence or parts thereof. Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode for polypeptides having at least 1, preferably at least 2, preferably at least three different amino acid residues compared to the published *H. pylori* counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucleic acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of the present invention according to the above outlined first, second, and third alternative. Stringent hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of the nucleic acid molecules according to any nucleic acid molecule of the present invention according to the first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers to the fact that preferably the nucleic acids according to the present invention code for the hyperimmune serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic acid molecule is particularly useful in the detection of a nucleic acid molecule according to the present invention and thus the diagnosis of the respective microorganisms such as *H. pylori* and any disease or diseased condition where this kind of microorganim is involved. Preferably, the hybridisation would occur or be preformed under stringent conditions as described in connection with the fourth alternative described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule or deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, nucleic acid molecule as used herein refers to, among other, single-and double-stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regions

comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecule" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules often referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are often used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragments, both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing of the *H. pylori* coding regions, which can be generated by standard cloning methods. To be unique, a fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any selected *H. pylori* fragment to the nucleotide sequences in computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *H. pylori* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deducted *H. pylori* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or

additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *H. pylori* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *H. pylori* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. {Tourdot, S. et al., 2000}, as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *H. pylori*, but trigger the same or preferably an improved T cell response. These epitope are referred to as "heteroclitic"; they need to have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999}, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by {Hemmer, B. et al., 1999} and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidemimetica" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instance, nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the nucleic acid molecules of the present invention. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, and may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have 50 bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated by screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents and materials for development of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to nucleic acid molecule assays, *inter alia*.

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the processes herein as described, but preferably for PCR, to determine whether or not the *H. pylori* genes identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. For this and other purposes the arrays comprising at least one of the nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nucleic acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundance of *H. pylori*.

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with *H. pylori* may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *H. pylori* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *H. pylori*, comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, Rnase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the nucleic acids can be isolated from *H. pylori* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification method. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 181-182, 194, 197-199, 206-207, 211-216, 219-220, 222, 226-230, 233, 235-236, 239, 241, 243, 245-246, 250, 252-253, 259, 262, 269, 272, 274-275, 279, 283-286, 290, 293-295, 297, 301-356 and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens, which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 186-188, 191-193, 195-196, 202, 205, 210, 217-218, 223-225, 234, 237, 240, 247-248, 251, 255, 257, 260, 263-264, 266, 268, 281, 287-288, 292, 299 and fragments thereof are provided. In a still preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 183, 185, 208-209, 231, 238, 244, 254, 261, 265, 270, 277, 298 and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactive antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to an antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide which retains essentially the same or a similar biological function or activity as such hyperimmune serum reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof may be 1) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of the amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune serum reactive antigen or fragment thereof is fused with another compound, such as a compound to increase the half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethylene glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune serum reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which is employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Among the particularly preferred embodiments of the invention in this regard are the hyperimmune serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypeptides

comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments are also encompassed by the present invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, can readily be made using standard techniques, including standard recombinant techniques for producing and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *H. pylori* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present

invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of a hyperimmune serum-reactive antigen are selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa", and "Location of identified immunogenic region" of Table 1, especially peptides comprising amino acids 63-91, 95-101, 110-116, 134-148, 150-156, 158-164, 188-193, 197-209, 226-241, 247-254, 291-297, 312-319, 338-346, 351-358, 366-378, 404-410, 420-438, 448-454, 465-473, 482-488, 490-498, 503-510, 512-519, 531-543, 547-554, 568-575, 589-604, 610-631 and 239-308 of Seq ID No 179; 16-29, 35-47, 50-68, 70-79, 91-101, 143-149, 158-163, 185-191, 196-206, 215-224, 230-237, 244-251, 258-278, 290-311, 319-325, 338-351, 365-385, 396-429, 445-454, 458-466, 491-499, 501-521, 17-79 and 218-233 of Seq ID No 180; 4-10, 16-41, 46-66, 77-84, 91-97, 102-118, 125-144, 187-200, 202-214, 245-253, 255-261, 286-295, 300-330, 335-342, 350-361, 363-381, 385-392, 396-416, 435-450 and 460-470 of Seq ID No 181; 11-19, 27-48, 52-59, 77-82, 84-107, 118-125, 127-154, 178-183, 192-209, 215-221, 286-295, 302-313, 350-357, 402-415, 417-431, 453-463, 465-493 and 313-331 of Seq ID No 182; 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All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or fragment thereof according to the present invention. Generally, any vector suitable to maintain, propagate or express nucleic acids to express a polypeptide in a host may be used for expression in this regard. In accordance with this aspect of the invention the vector may be, for example, a plasmid vector, a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starting plasmids disclosed herein are either commercially available, publicly available, or can be constructed from available plasmids by routine application of well-known, published procedures. Preferred among vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune serum reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic acid molecules of the present invention. Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, *E. coli*, *Streptomyces* and *Bacillus subtillis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, Hela, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *H. pylori* hyperimmune serum reactive antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reactive antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invention. The invention further provides a process for producing a cell, which expresses a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfecting a suitable host cell with the vector according to the present invention such that the transformed or transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, regions may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. et al., 1995} and {Johanson, K. et al., 1995}.

The *H. pylori* hyperimmune serum reactive antigen or a fragment thereof can be recovered and purified

from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention can be produced by chemical synthesis as well as by biotechnological means. The latter comprise the transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease, most preferably for the diagnosis of diseases related or linked to the presence or abundance of Gram-negative bacteria, especially bacteria selected from the group comprising Helicobacter, Campylobacter and Arcobacter. More preferably, the microorganisms are selected from the group comprising *Helicobacter cinaedi* and *Helicobacter fanneliae*, especially the microorganism is *Helicobacter pylori*.

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per cm^2 is in a preferred embodiment as little as 10 peptides/polypeptides per cm^2 to at least 400 different peptides/polypeptides per cm^2 and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per cm^2.

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the generation of an array as described above. This applies as well to an array made of antibodies, preferably monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmune serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the present invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expression library. It is within the present invention that the antibody may be chimeric, i. e. that different parts thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments thereof corresponding to a sequence of the present invention can be obtained by direct injection of the hyperimmune serum reactive antigens and fragments thereof into an animal or by administering the hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. The antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments thereof itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum reactive antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmune serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate the hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmune serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibodies produced by continuous cell line cultures can be used. (as described originally in {Kohler, G. et al., 1975}.

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody genes with binding activities towards the hyperimmune serum reactive antigens and fragments thereof either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing respective target antigens or from naïve libraries {McCafferty, J. et al., 1990}; {Marks, J. et al., 1992}. The affinity of these antibodies can also be improved by chain shuffling {Clackson, T. et al., 1991}.

If two antigen binding domains are present, each domain may be directed against a different epitope – termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum reactive antigens and fragments thereof of the present invention by attachment of the antibody to a solid support for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments thereof of the present invention may be employed to inhibit and/or treat infections, particularly bacterial infections and especially infections arising from *H. pylori*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopically or immunologically equivalent derivatives, which form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive antigen and fragments thereof or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}, {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently

be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about 10^2 to 10^{18}, preferably 10^8 to 10^{15} different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the so-called "anticalines" which are, among others, described in the German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifically interact with a target molecule. The manufacture or selection of aptamers is, e. g., described in European patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. e. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of several, preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted with the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increased affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The binding nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the thus obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeated several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding to the target from which the final binding nucleic acid is then optionally selected. These specifically binding nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generation or identification of the aptamers samples of the mixture of individual nucleic acids may be taken to determine the sequence thereof using standard techniques. It is within the present invention that the aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known to the one skilled in the art of generating aptamers. Such modification may for example reside in the introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers are currently used as therapeutical agents. However, it is also within the present invention that the thus selected or generated aptamers may be used for target validation and/or as lead substance for the development of medicaments, preferably of medicaments based on small molecules. This is actually done by a competition assay whereby the specific interaction between the target molecule and the aptamer is inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target and aptamer it may be assumed that the respective drug candidate allows a specific inhibition of the interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at least in principle, be suitable to block the target and thus decrease its biological availability or activity in a respective system comprising such target. The thus obtained small molecule may then be subject to further derivatisation and modification to optimise its physical, chemical, biological and/or medical characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufacture of spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nucleic acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers are. Spiegelmers are characterized by the fact that they have a very high stability in biological systems and, comparable to aptamers, specifically interact with the target molecule against which they are directed. In

the process of generating spiegelmers, a heterogeonous population of D-nucleic acids is created and this population is contacted with the optical antipode of the target molecule, in the present case for example with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic acids are separated which do not interact with the optical antipode of the target molecule. But those D-nucleic acids interacting with the optical antipode of the target molecule are separated, optionally identified and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based on the nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids which are identical in terms of sequence with the aforementioned D-nucleic acids interacting with the optical antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids, which preferably consist of RNA which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in {Doherty, E. et al., 2001} and {Lewin, A. et al., 2001}.

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybride complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed base on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a

minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2'-O-methyl or 2'-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5'→3'-linked nucleotides. Rather the oligonucleotides have two types of nucleotides: 2'-deoxyphosphorothioate, which activate RNase H, and 2'-modified nucleotides, which do not. The linkages between the 2'-modified nucleotides can be phosphodiesters, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating region, which contains between 3 and 5 2'-deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2'- deoxyphosphorothioate nucleotides to activate eucaryotic and, particularly, mammalian RNase H. Protection from degradation is accomplished by making the 5' and 3' terminal bases highly nuclease resistant and, optionally, by placing a 3' terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5' terminus and a 3' terminus; and from position 11 to 59 5'→3'-linked nucleotides independently selected from the group consisting of 2'-modified phosphodiester nucleotides and 2'-modified P-alkyloxyphosphotriester nucleotides; and wherein the 5'-terminal nucleoside is attached to an RNase H-activating region of between three and ten contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3'-terminus of said oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguous stretch of one to three phosphorothioate 2'-modified ribonucleotides, a biotin group and a P-alkyloxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5' terminal nucleoside is attached to an RNase H-activating region but the 3' terminal nucleoside as specified above. Also, the 5' terminus is selected from the particular group rather than the 3' terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used as or for the manufacture of pharmaceutical compositions, especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the prevention or treatment of diseases caused by, related to or associated with *H. pylori*. In so far another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, which comprises inoculating the individual with the hyperimmune serum reactive antigens and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibodies to protect said individual from infection, particularly *Helicobacter* infection and most particularly *H. pylori* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in an individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functionally encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a cell mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced into a

host capable of having induced within it an immunological response, induces an immunological response in such host, wherein the composition comprises recombinant DNA which codes for and expresses an antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment thereof may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular fragments thereof in such genetic immunization experiments in animal models of infection with *H. pylori*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *H. pylori* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue caused e.g. by mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or tramsdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *H. pylori*. Such a pharmaceutical composition may comprise one or more hyperimmune serum reactive antigens or fragments thereof against *H. pylori*. Optionally, such *H. pylori* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *H. pylori* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *H. pylori*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *H. pylori*. Optionally, such *H. pylori* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *H. pylori* and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buffer substances, stabilisers or further active ingredients, especially ingredients known in connection of pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or a coding nucleic acid molecule thereof according to the present invention is an immunostimulatory compound for further stimulating the immune response to the given hyperimmune serum-reactive antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulatory compound in the pharmaceutical preparation according to the present invention is selected from the group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic acids molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvants, Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, or combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic polyppetides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database under the following internet address:

http://www.bbcm.univ.trieste.it/~tossi/pag2.html

Such host defence peptides or defensives are also a preferred form of the polycationic polymer according

to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorporated herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, preferably from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide, which has the amino acid sequence NH_2-RLAGLLRKGGEKIGEKLKKIGOKIKNFFQKLVPQPE-COOH. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids, which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferablly, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO 01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof:

the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % by weight of the formulation; more usually they will constitute up to about 80 % by weight of the formulation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μg antigen / per kg of body weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compounds of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulation or combination. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. use of the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which is caused by, linked or associated with Helicobacter, more preferably, *H. pylori*. In connection therewith it is

to be noted that *H. pylori* comprises several strains including those disclosed herein. A disease related, caused or associated with the bacterial infection to be prevented and/or treated according to the present invention includes besides others peptic ulcer and assoziated cancer in humans.

In a still further embodiment the present invention is related to a screening method using any of the hyperimmune serum reactive antigens or nucleic acids according to the present invention. Screening methods as such are known to the one skilled in the art and can be designed such that an agonist or an antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prevents the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist) or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its acitivity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding

molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see {Okano, H. et al., 1991}; OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Boca Ration, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens and fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according to the present invention is its capability to bind to any of its interaction partner or the extent of such capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens and fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: i) in the prevention of adhesion of *H. pylori* to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in mucosal wounds; ii) to block protein mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases {Rosenshine, I. et al., 1992} to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins which mediate tissue damage; iv) to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

Each of the DNA coding sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infection with Helicobacter, especially *H. pylori*, such as peptic ulcer disease and gastric cancer.

In a still further aspect the present invention is related to an affinity device such affinity device comprises as least a support material and any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, which is attached to the support material. Because of the specificity of the hyperimmune serum reactive antigens and fragments thereof according to the present invention for their target cells or target molecules or their interaction partners, the hyperimmune serum reactive antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kind of sample applied to the support material provided that the conditions for binding are met. The sample may be a biological or medical sample, including but not limited to, fermentation broth, cell debris, cell preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix in a covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and can

be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, starch and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence listing from which further features, embodiments and advantages may be taken. It is to be understood that the present examples are given by way of illustration only and not by way of limitation of the disclosure.

In connection with the present invention

Figure 1 shows the characterization of *H. pylori* specific human sera.

Figure 2 shows the characterization of the small fragment genomic library LHP1-50 from *H. pylori* isolate KTH-Ca1.

Figure 3 shows the characterization of the small fragment genomic library LHP2-50 from *H. pylori* isolate KTH-Du.

Figure 4 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Table 1 shows the summary of all screens performed with genomic *H. pylori* libraries and human serum.

The figures to which it might be referred to in the specification are described in the following in more details.

Figure 1 shows the characterization of human sera for anti-*H. pylori* antibodies as measured by immune assays. Total anti- *H. pylori* IgG and IgA antibody levels were measured by standard ELISA using total bacterial lysate prepared from *H. pylori* KTH Ca1 strain as coating antigen. **(A)** Serum samples from randomly selected 54 adults were analysed for antibody levels and afterwards interviewed for symptoms (gasctric pain) and previous history of *H. pylori* infections. Four individuals were identified with high antibody titers without symptoms or disease (S-) and four with acute symptoms or known clinical disease (S+). **(B)** Sera from patients presenting themselves with typical symptoms of *H. pylori* diseases were analysed for IgG and IgA levels and grouped based on negative or positive results in the Urease test performed by clinicians. ELISA units are calculated from absorbance readings at two serum dilutions (10.000X and 50.000X). Averages for the two different groups are given. **(C)** Immunoblot analysis was performed on sera pre-selected by ELISA in order to ensure multiple immune reactivity with protein antigens. Results of a representative experiment using total bacterial lysate prepared from *H. pylori* KTH Ca1 strain and selected sera at 5.000X dilution are shown. Serum samples are from; Lane 1: a high titer S- individual, Lane 2: a high titer urease -patient, Lane 3 and 4: a high titer urease + patient. Lane 1-3 was developed with anti-human IgG secondary antibody and Lane 4 with anti-human IgA secondary antibody. Mw: molecular weigth markers.

Figure 2 shows the fragment size distribution of the KTH-Ca1 *H. pylori* strain small fragment genomic library, LHP1-50. After sequencing 576 randomly selected clones sequences were trimmed to eliminate vector residues and the number of clones with various genomic fragment sizes were plotted. **(B)** Graphic illustration of the distribution of the same set of randomly sequenced clones of LHP1-50 over the *H. pylori* chromosome. Blue circles indicate matching sequences to annotated ORFs in both +/+ and +/- orientations. Red rectangles represent fully matched clones to non-coding chromosomal sequences in both +/+ and +/- orientations. Green diamonds positions all clones with chimeric sequences. Numeric distances in base pairs are indicated over each circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 3 shows the fragment size distribution of the KTH-Du *H. pylori* strain small fragment genomic library, LHP2-50. After sequencing 576 randomly selected clones sequences were trimmed to eliminate vector residues and the number of clones with various genomic fragment sizes were plotted. (B) Graphic illustration of the distribution of the same set of randomly sequenced clones of LHP2-50 over the *H. pylori* chromosome. Blue circles indicate matching sequences to annotated ORFs in both +/+ and +/- orientations. Red rectangles represent fully matched clones to non-coding chromosomal sequences in both +/+ and +/- orientations. Green diamonds positions all clones with chimeric sequences. Numeric distances in base pairs are indicated over each circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 4A shows the MACS selection with biotinylated human IgGs. The LHP1-50 library in pMAL9.1 was screened with 10 μg biotinylated, human serum (P6-IgG) in the first and with 10 μg in the second selection round. As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1^{st} and 2^{nd} elution are shown for each selection round. Figure 4B shows the reactivity of specific clones (1-26) isolated by bacterial surface display as analysed by Western blot analysis with the human serum (P6-IgG) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000. LB, Extract from a clone expressing LamB without foreign peptide insert.

Table 1: Immunogenic proteins identified by bacterial surface display.
A, 300bp library of *H. pylori* KTH Ca1 in fhuA with IC7-IgG (757), B, 300bp library of *H. pylori* KTH Ca1 in fhuA with P5-IgG (729), C, 300bp library of *H. pylori* KTH Ca1 in fhuA with P9-IgG (441), D, 50bp library of *H. pylori* KTH Ca1 in lamB with IC7-IgG (448), E, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgA (1130), F, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgG (911), G, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgA (1135), H, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgG (844), I, 50bp library of *H. pylori* KTH Ca1 in lamB with P9-IgG (1121), J, 300bp library of *H. pylori* KTH Du in fhuA with P6-IgG (433), K, 300bp library of *H. pylori* KTH Du in fhuA with P8-IgG (550), L, 50bp library of *H. pylori* KTH Du in lamB with P6-IgG (1077), M, 50bp library of *H. pylori* KTH Du in lamB with P8-IgG (740); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC {Kolaskar, A. et al., 1990}.

EXAMPLES

Example 1: Characterization and selection of human sera based anti-*H.pylori* antibodies, preparation of antibody screening reagents

Experimental procedures

Enzyme linked immune assay (ELISA).
ELISA plates (Maxisorb, Millipore) were coated with 5-10 μg/ml total protein diluted in coating buffer (0.1M sodium carbonate pH 9.2). Three dilutions of sera (2,000X, 10,000X, 50,000X) were made in PBS-BSA. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG or anti-human IgA secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Antigen-antibody complexes were quantified by measuring the conversion of the substrate (ABTS) to colored product based on OD_{405nm} readings by automatic ELIAS reader (TECAN SUNRISE).

Preparation of bacterial antigen extracts
H. pylori KTH DU or KTH Ca1 strains were grown for 48 hours on agar plates, cells collected and lysed by repeated freeze-thaw cycles: incubation on dry ice/ethanol-mixture until frozen (1 min), then thawed at 37°C (5 min): repeated 3 times. This was followed by sonication and collection of supernatant by centrifugation (3,500 rpm, 15 min, 4°C).

Immunoblotting
Total bacterial lysate preparations were prepared from *in vitro* grown *H. pylori* KTH DU or KTH Ca1 strains. 10 to 25µg total protein/lane was separated by SDS-PAGE using the BioRad Mini-Protean 3 Cell electrophoresis system and proteins transferred to nitrocellulose membrane (ECL, Amersham Pharmacia). After overnight blocking in 5% milk, human sera were added at 2,000x dilution, and HRPO labeled anti-human IgG was used for detection.

Purification of antibodies for genomic screening. Five sera from both the patient and the healthy group were selected based on the overall anti-streptococcal titers for a serum pool used in the screening procedure. Antibodies against *E. coli* proteins were removed by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pHIE11, grown under the same condition as used for bacterial surface display). Highly enriched preparations of IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, according to the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). IgA antibodies were purified also by affinity chromatography using biotin-labeled anti-human IgA (Southern Biotech) immobilized on Streptavidin-agarose (GIBCO BRL). The efficiency of depletion and purification was checked by SDS-PAGE, Western blotting, ELISA and protein concentration measurements.

Results

The antibodies produced against *H. pylori* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. These molecules are essential for the identification of individual antigens in the approach as described in the present invention, which is based on the interaction of the specific antibodies and the corresponding *H. pylori* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from

I. 54 randomly selected healthy adults. Individuals were interviewed for the presence or absence of clinical symptoms and previously diagnosed *H. pylori* infection.
II. patients with duodenal ulcer.
III. patients with gastric ulcer and cancer.

For the patient groups *H. pylori* infection was confirmed and medical diagnosis was based on medical microbiological tests, Urease test, biopsy or gastroscopy. A total of 191 sera from patients were included in the analysis.

The sera were characterized for anti-*H. pylori* antibodies by a series of ELISA and immunoblotting assays. For that purpose two different antigen preparation were used: whole cell extracts prepared from *H. pylori* strains KTH-Ca1 and KTH-Du and both IgG and IgA antibody levels were determined. Antibody titers were expressed as units calculated from absorbance readings at two different dilutions - 10.000X and 50.000X for IgG and 1.000X and 5.000X for IgA - where the response was linear (Fig 1A and B). Among the high titer randomly taken individuals eigth out of the 54 included (15%) showed significant IgG and IgA antibody levels. Half of these individuals were known *H. pylori* 'patients' acutely or before, the other half had no medical history or any complains. Sera of these four individuals were pooled and prepared for antigen identification. Since *H. pylori* infections are common, antibodies are present as a consequence of natural immunization from previous encounters with *Helicobacter* even without consequent carriage. The value of the ELISA assay imployed were further proved by analyzing patients' sera with or without active disease. Comparing the antibody levels in urease test positive and urease test negative individuals,

significantly higher antibody levels were measured in the Urease + group (Fig. 1B). According to literature data, the false negative cases (~ 10%) are much more prevalent then the false positives in this test, suggesting that the ELIAS assays is likely to be even more powerful predicting active *H. pylori* infections. Sera were ranked based on the reactivity against total lysate preparation in both antibody classes, and the highest ones from all three serum donor groups were selected for further analysis by immunoblotting. This latter assay confirmed immune reactivity against multiple *H. pylori* proteins, as it is examplified on Fig. 1C.

This extensive antibody characterization approach has led to the unambiguous identification of anti-*Helicobacter* hyperimmune sera and allowed the preparation of 5 donor pools.

Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Helicobacter pylori*

Experimental procedures

Preparation of helicobacter genomic DNA. Sufficient amounts of bacterial pellets from the KTH-Ca1 and KTH-Du clinical isolates of *H. pylori* were obtained from Dr. Lars Engstrand. Bacterial pellets were washed 3 x with PBS and carefully re-suspended in 0.5 ml of Lysozyme solution (100 mg/ml). 0.1 ml of 10 mg/ml heat treated RNase A and 20 U of RNase T1 were added, mixed carefully and the solution was incubated for 1 h at 37°C. Following the addition of 0.2 ml of 20 % SDS solution and 0.1 ml of Proteinase K (10 mg/ml) the tube was incubated overnight at 55 °C. 1/3 volume of saturated NaCl was then added and the solution was incubated for 20 min at 4°C. The extract was pelleted in a microfuge (13,000 rpm) and the supernatant transferred into a new tube. The solution was extracted with PhOH/$CHCl_3$/IAA (25:24:1) and with $CHCl_3$/IAA (24:1). DNA was precipitated at room temperature by adding 0.6x volume of Isopropanol, spooled from the solution with a sterile Pasteur pipette and transferred into tubes containing 80% ice-cold ethanol. DNA was recovered by centrifuging the precipitates with 10-12,000x g, then dried on air and dissolved in ddH_2O.

Preparation of small genomic DNA fragments. Genomic DNA was mechanically sheared into fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV 2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DN*ase* I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DN*ase* I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DN*ase* I provided with the kit was prepared and the digestion was performed in the presence of $MnCl_2$ in a 60 µl volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 µl of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twice using T4 DNA Polymerase in the presence of 100 µM each of dNTPs to ensure efficient flushing of the ends. Fragments were used immediately in ligation reactions or frozen at -20°C for subsequent use.

Description of the vectors. The vector pMAL4.31 was constructed on a pASK-IBA backbone (Skerra, A., 1994) with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition, the *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase is preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasmic membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature beta-

lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after the leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region would decrease or abolish translocation across the cytoplasmic membrane {Kajava, A. et al., 2000}. A *Sma*I restriction site serves for library insertion. An upstream FseI site and a downstream NotI site, which were used for recovery of the selected fragment, flank the *Sma*I site. The three restriction sites are inserted after the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed in the -1 reading frame resulting in a stop codon 15 bp after the *Not*I site. A +1 bp insertion restores the *bla* ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pEH1 {Hashemzadeh-Bonehi, L. et al., 1998}. Subsequently, a sequence was inserted in *lamB* after amino acid 154, containing the restriction sites *Fse*I, *Sma*I and *Not*I. The reading frame for this insertion was constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pEH1. Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *Fse*I, *Xba*I and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *fhuA* and the respective insert.

Cloning and evaluation of the library for frame selection. Genomic fragments of *H.pylori* DNA were ligated into the *Sma*I site of the vector pMAL4.31. Recombinant DNA was electroporated into DH10B electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented with Kanamycin (50 μg/ml) and Ampicillin (50 μg/ml). Plates were incubated over night at 37°C and colonies collected for large scale DNA extraction. A representative plate was stored and saved for collecting colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was used to initially determine the rough fragment size distribution as well as insertion efficiency. From sequencing data the precise fragment size was evaluated, junction intactness at the insertion site as well as the frame selection accuracy (3*n*+1 *rule*).

Cloning and evaluation of the library for bacterial surface display. Genomic DNA fragments were excised from the pMAL4.31 vector, containing the *H. pylori* libraries with the restriction enzymes *Fse*I and *Not*I. The entire population of fragments was then transferred into plasmids pMAL9.1 (LamB) or pHIE11 (FhuA), which have been digested with *Fse*I and *Not*I. Using these two restriction enzymes, which recognise an 8 bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in each of the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells by electroporation. Cells were plated onto large LB-agar plates supplemented with 50 μg/ml Kanamycin and grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scraped off the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening at -80°C.

Results

Libraries for frame selection. Four libraries (LHP1-50, LHP2-50, LHP1-300 and LHP2-300) were generated in the pMAL4.31 vector with sizes of approximately 50 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 μg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *H. pylori* DNA yielded 4x 10^5 to 2x 10^6 clones after frame selection. To assess the randomness of the libraries, approximately 600 randomly chosen clones of LHP1-50 and LHP2-50 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown for example for LHP2-50 that 90% of the clones fell in the size range

between 19 and 64 bp with an average size of 28 bp (Figure 2, 3). All sequences followed the *"3n+1 rule"*, showing that all clones were properly frame selected.

Bacterial surface display libraries. The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LHP libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *Fse*I and *Not*I restriction and ligation of 5ng inserts with 0.1μg plasmid DNA and subsequent transformation into DH5alpha cells resulted in 2-5x 10^6 clones. The clones were scraped off the LB plates and frozen without further amplification.

Example 3: Identification of highly immunogenic peptide sequences from *H. pylori* using bacterial surface displayed genomic libraries and human serum

Experimental procedures

MACS screening. Approximately 2.5x 10^8 cells from a given library were grown in 5 ml LB-medium supplemented with 50 μg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2x 10^7 cells re-suspended in 100 μl LB medium and transferred to an Eppendorf tube.

10 μg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated over night at 4°C with gentle shaking. 900 μl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (for IgA screens, 10 μg of purified IgAs were used and these captured with biotinylated anti-human-IgA secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 μl LB medium. 10 μl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 μl of LB medium was added and the MACS microbead cell suspension was loaded onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 μg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min. Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 μl LB medium. Since the volume was reduced, 10 μg of human, biotinylated IgGs was added and the suspension incubated over night at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were plated onto LB-agar plates supplemented with 50 μg/ml Kanamycin and grown over night at 37°C.

Evaluation of selected clones by sequencing and Western blot analysis. Selected clones were grown over night at 37°C in 3 ml LB medium supplemented with 50 μg/ml Kanamycin to prepare plasmid DNA using standard procedures. Sequencing was performed at MWG (Germany).

For Western blot analysis approximately 10 to 20 μg of total cellular protein was separated by 10% SDS-PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB or FhuA fusion proteins were detected using human serum as the primary antibody at a dilution of

approximately 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 as secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharmacia Biotech, England). Alternatively, rabbit anti FhuA or mouse anti LamB antibodies were used as primary antibodies in combination with the respective secondary antibodies coupled to HRP for the detection of the fusion proteins.

Results

Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated Igs. The libraries LHP1-50 and LHP2-50 in pMAL9.1 and LHP1-300 and LHP2-300 in pHIE11 were screened with pools of biotinylated, human IgGs and IgAs from patient sera or sera from healthy individuals (see Example 1: *Preparation of antibodies from human serum*). The selection procedure was performed as described under Experimental procedures. Figure 4A shows a representative example of a screen with the LHP1-50 library and P6-IgGs. As can be seen from the colony count after the first selection cycle from MACS screening, the total number of cells recovered at the end is reduced from app. 1 to 2x 10^7 cells to approximately 10^4 cells, whereby the selection in the presence of serum yielded a slightly higher number of cells than in the absence of antibodies (Figure 4A). After the second round of screening however, a similar number of cells was recovered with P6-IgG, while only a few hundred cells were recovered when no IgGs from human serum were added, clearly showing that selection was dependent on *H. pylori* specific antibodies. To evaluate the performance of the screen, approximately 50 selected clones were picked randomly and subjected to Western blot analysis with the same, pooled serum (Figure 4B). This analysis revealed that 70% of the selected clones showed reactivity with antibodies present in the relevant serum whereas the control strain expressing LamB without a *H. pylori* specific insert did not react with the same serum. In general, the rate of reactivity was observed to lie within the range of 35 to 75%. Colony PCR analysis confirmed that all selected clones contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 1200 per screen) led to the identification of the gene and the corresponding peptide or protein sequence that was specifically recognized by the human serum used for screening. The frequency with which a specific clone is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the serum used for selection and recognizing the epitope presented by this clone. In that regard it is striking that clones derived from some ORFs (e.g. HP0527, HP0547 and HP1341) were picked more than 100 times, indicating their highly immunogenic property. Table 1 summarizes the data obtained for all 13 performed screens. All clones in Table 1 have been verified by Western blot analysis with whole cellular extracts from single clones to show the indicated reactivity with the pool of human serum used in the respective screen. As seen in Table 1, distinct regions of the identified ORF are identified as immunogenic, since variably sized fragments of the proteins are displayed on the surface by the platform proteins.

It is further worth noticing that most of the genes identified by the bacterial surface display screen encode proteins that are either attached to the surface of *H. pylori* and/or are secreted. This is in accordance with the expected role of surface attached or secreted proteins in virulence of *H. pylori.*

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Table 1: Immunogenic proteins identified by bacterial surface display.

A, 300bp library of *H. pylori* KTH Ca1 in fhuA with IC7-IgG (757), B, 300bp library of *H. pylori* KTH Ca1 in fhuA with P5-IgG (729), C, 300bp library of *H. pylori* KTH Ca1 in fhuA with P9-IgG (441), D, 50bp library of *H. pylori* KTH Ca1 in lamB with IC7-IgG (448), E, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgA (1130), F, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgG (911), G, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgA (1135), H, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgG (844), I, 50bp library of *H. pylori* KTH Ca1 in lamB with P9-IgG (1121), J, 300bp library of *H. pylori* KTH Du in fhuA with P6-IgG (433), K, 300bp library of *H. pylori* KTH Du in fhuA with P8-IgG (550), L, 50bp library of *H. pylori* KTH Du in lamB with P6-IgG (1077), M, 50bp library of *H. pylori* KTH Du in lamB with P8-IgG (740); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990).

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP0009	outer membrane protein (omp1)	63-91,95-101,110-116,134-148,150-156,158-164,188-193,197-209,226-241,247-254,291-297,312-319,338-346,351-358,366-378,404-410,420-438,448-454,465-473,482-488,490-498,503-510,512-519,531-543,547-554,568-575,589-604,610-631	G: 1, H: 2, K: 2, M: 38	239-308	1, 179
HP0010	chaperone and heat shock protein (groEL)	16-29,35-47,50-68,70-79,91-101,143-149,158-163,185-191,196-206,215-224,230-237,244-251,258-278,290-311,319-325,338-351,365-385,396-429,445-454,458-466,491-499,501-521	K: 1	17-79, 218-233	2, 180
HP0043	mannose-6-phosphate isomerase (pmi)	4-10,16-41,46-66,77-84,91-97,102-118,125-144,187-200,202-214,245-253,255-261,286-295,300-330,335-342,350-361,363-381,385-392,396-416,435-450	G: 1	460-470	3, 181
HP0063	hypothetical protein	11-19,27-48,52-59,77-82,84-107,118-125,127-154,178-183,192-209,215-221,286-295,302-313,350-357,402-415,417-431,453-463,465-493	D: 4, E: 1, G: 2	313-331	4, 182
HP0067	urease accessory protein (ureH)	19-26,30-43,47-55,63-68,72-80,97-104,107-119,129-146,160-175,194-216,231-251,254-260	H: 1	26-43	5, 183
HP0072	urease beta subunit (urea amidohydrolase) (ureB)	7-13,29-37,65-81,110-120,123-131,135-152,230-249,254-260,284-290,292-299,317-326,329-336,403-444,452-458,466-477,490-498,510-519,541-550,557-566	E: 2, G: 3, H: 1, M: 2	533-567	6, 184
HP0086	Conserved hypothetical protein	5-47,71-77,79-86,89-95,120-126,137-144,176-181,184-196,202-208,211-232,236-282,301-313,317-325,341-347,353-384,394-400,412-433,436-443	B: 3, C: 1, I: 4	59-75	7, 185
HP0087	hypothetical protein	4-18,22-38,59-69,106-112,116-130,138-149,156-	A: 2, B: 2,	1-104, 130-147	8, 186

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		170,175-197,200-214,216-223,233-244,255-261,266-276,279-286,325-333,342-348,366-399,402-420,429-441	E: 2, F: 1, G: 2, I: 1, L: 2		
HP0088	RNA polymerase sigma-70 factor (rpoD)	50-58,69-95,97-113,131-136,157-163,170-175,188-212,220-226,254-259,265-277,283-289,297-308,311-318,347-358,360-369,378-401,416-421,440-450,454-462,470-476,493-502,506-514,536-567,585-590,598-607,613-618,653-659	A: 2, B: 9, D: 2, F: 3, H: 4	35-46	9, 187
HP0089	pfs protein (pfs)	16-29,32-60,65-87,89-123,128-134,137-158,162-173,178-196,210-216,218-228	E: 11, G: 2	206-225	10, 188
HP0115	flagellin B (flaB)	10-20,26-35,51-64,86-91,94-100,113-122,154-160,185-191,193-201,211-217,225-230,237-246,251-257,298-304,306-312,316-328,340-348,357-389,391-397,415-421,449-456,458-471,488-495,502-511	F: 2, H: 1, K: 1, L: 52	24-55, 236-341	11, 189
HP0175	cell binding factor 2	5-22,41-51,87-93,114-122,127-136,150-156,158-166,223-233,245-263,291-296	A: 11, C: 7, K: 2	9-126, 127-285	12, 190
HP0121	phosphoenolpyruvate synthase (ppsA)	30-43,46-56,61-70,72-83,85-93,103-113,119-125,151-166,179-191,212-218,225-231,236-243,262-267,291-307,331-344,349-355,366-372,380-386,414-422,428-447,459-464,469-478,507-519,525-544,563-569,576-590,620-626,633-643,654-659,665-671,684-707,717-723,725-733,747-779,782-801	H: 3, I: 4, K: 3	347-361	13, 191
HP0123	threonyl-tRNA synthetase (thrS)	4-12,14-26,37-80,107-115,133-139,144-150,154-165,173-180,191-199,205-211,221-231,237-244,254-284,307-340,342-353,360-368,370-380,479-493,495-503,509-522,525-536,539-547,554-560,565-573,578-583	D: 6, F: 1, H: 2, M: 1	7-23, 465-479	14, 192
HP0130	hypothetical protein	4-17,47-55,76-83,85-100,104-112,117-123,126-135,142-148,156-167,174-182,267-273	A: 1, C: 1, I: 1, K: 1, M: 3	258-283	15, 193
HP0150	hypothetical protein	8-32,36-42,65-88,102-108,112-140,147-163,170-179,183-193	A: 1, B: 1, D: 1, J: 1, L: 2	117-124	16, 194
HP0183	serine hydroxymethyltransferase (glyA)	12-18,45-50,62-77,82-95,99-113,115-123,125-147,155-177,187-209,211-223,244-253,259-270,278-297,302-307,311-318,329-334,350-356,359-365,390-400,402-413	I: 5	333-350	17, 195
HP0192	fumarate reductase,	4-13,15-27,30-46,53-58,68-74,82-95,115-126,134-	H : 1, I :	376-400	18, 196

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	flavoprotein subunit (frdA)	139,148-153,159-176,182-199,201-217,220-225,227-235,237-248,253-266,300-315,322-336,390-396,412-426,438-445,448-459,477-484,502-508,515-527,529-537,553-568,643-651,658-667,690-703	4, L: 20		
HP0197	S-adenosylmethionine synthetase 2 (metX)	4-10,24-32,38-55,59-67,70-77,80-87,89-97,123-129,134-151,166-172,178-189,191-216,218-235,245-259,271-315,326-339,341-360	F: 1, H: 1, L: 8	73-94	19, 197
HP0201	fatty acid/phospholipid synthesis protein (plsX)	13-25,31-38,43-57,79-85,92-99,106-112,117-128,130-139,146-158,160-175,194-204,211-222,225-232,234-242,263-270,278-292,299-320,322-333	L: 5	240-256	20, 198
HP0202	beta-ketoacyl-acyl carrier protein synthase III	4-17,55-63,66-101,109-131,135-143,145-151,155-161,164-170,177-185,192-198,213-218,223-238,246-256,258-268,273-283,309-314,322-328	F: 1, I: 3	195-221	21, 199
HP0210	chaperone and heat shock protein C62.5 (htpG)	13-24,31-39,41-50,63-69,90-96,104-109,116-141,148-153,161-167,173-178,190-209,253-258,265-272,279-289,295-312,317-343,355-366,376-389,400-407,430-451,453-464,466-472,487-493,499-505,523-538,554-559,568-579,584-601	F: 1, M: 2	344-363	22, 200
HP0211	conserved hypothetical secreted protein	5-22,30-36,53-59,61-70,82-92,99-106,120-131,135-148,154-167,169-183,187-199,204-212,231-247	A: 1, C: 1, K: 1	111-249	23, 201
HP0228	conserved hypothetical integral membrane protein	17-36,40-66,71-144,148-171,173-191,199-214,220-252,265-272,278-288,298-333,342-385	A: 1, E: 6, F: 1	287-307	24, 202
HP0229	outer membrane protein (omp6)	4-16,22-28,30-36,42-48,95-116,154-162,164-174,239-252,258-263,273-285,306-313,323-333,341-357,363-369,372-379,395-401,430-436,438-453,464-480	E: 1, F: 1, L: 14	33-44, 233-258, 349-369	25, 203
HP0235	conserved hypothetical secreted protein	4-21,30-37,46-53,59-68,80-92,98-104,118-143,150-160,165-185,187-200,204-211,224-236,241-246,252-258,271-280,288-294,311-320,335-341	B: 5	191-350	26, 204
HP0239	glutamyl-tRNA reductase (hemA)	4-16,37-59,64-70,79-87,93-102,107-127,143-165,172-188,197-204,207-218,221-227,242-248,258-277,289-296,298-316,332-338,344-365,367-373,375-382,400-408,415-425,438-446	H: 2	235-250	27, 205
HP0258	conserved	4-37,39-66,84-98,101-127,140-149,157-163,166-	H: 1, L: 1	183-204	28, 206

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	hypothetical integral membrane protein	172,175-182,184-193,203-208,215-232,234-247,250-299,303-345			
HP0266	dihydroorotase (pyrC)	10-20,41-61,73-87,112-141,176-192,194-201,205-222,230-237,257-264,276-282,284-310,312-318,330-337,349-357	M: 21	304-328	29, 207
HP0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	4-31,42-103,105-113,121-153,160-181,188-196,210-226,231-264,272-287,297-304,328-336	G: 1, L: 6	304-318	30, 208
HP0289	toxin-like outer membrane protein	21-43,46-52,54-70,72-79,94-107,133-141,160-166,217-253,311-317,359-365,374-381,390-395,434-440,488-494,497-502,511-522,554-563,565-574,577-585,591-598,601-606,617-625,633-643,658-664,676-682,694-702,710-719,754-760,782-788,802-808,916-921,942-948,955-964,973-979,992-998,1006-1011,1016-1023,1030-1038,1046-1053,1059-1066,1088-1098,1119-1126,1129-1135,1156-1171,1173-1181,1202-1210,1255-1261,1268-1280,1295-1310,1312-1320,1375-1381,1406-1417,1450-1471,1478-1492,1498-1506,1569-1578,1603-1608,1611-1624,1648-1655,1663-1670,1680-1698,1702-1707,1713-1719,1737-1742,1747-1753,1762-1769,1771-1785,1790-1804,1811-1818,1830-1836,1838-1852,1874-1886,1893-1899,1902-1909,1942-1948,1952-1962,1980-1986,2001-2017,2020-2028,2042-2050,2052-2068,2074-2079,2083-2095,2107-2113,2147-2155,2177-2194,2203-2211,2236-2241,2251-2258,2267-2274,2285-2292,2314-2328,2330-2340,2358-2365,2390-2401,2408-2418,2432-2453,2463-2476,2486-2507,2528-2537,2540-2548,2552-2558,2568-2576,2596-2601,2610-2622,2629-2638,2653-2669,2718-2727,2749-2767,2777-2784,2789-2795,2806-2815,2817-2824,2835-2843,2847-2854,2860-2881	B: 1, E: 2, H: 2, I: 3, L: 7	511-523, 612-630, 1790-1803	31, 209
HP0292	hypothetical protein	4-54,61-68,72-82,86-93,100-108,115-130,147-154,187-194,196-207,224-229,236-251,275-287	E:14	96-109	32, 210
HP0295	flagellin B homolog	31-39,62-69,91-101,158-172,175-180,186-193,201-	A: 1, B: 2,	366-503	33, 211

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	(fla)	208,210-223,243-250,273-286,293-299,319-325,343-354,356-365,368-384,414-435,471-491,512-518,550-556,567-581,584-589,633-639,680-692,697-708,716-721,747-754,779-786,810-816	C: 3		
HP0349	CTP synthetase (pyrG)	5-20,22-48,57-65,96-101,111-122,130-145,154-164,170-181,193-199,201-216,224-241,244-262,281-323,342-351,359-367,369-396,406-416,424-433,450-456,485-491,493-499,501-515,517-535	M:2	289-305	34, 212
HP0351	flagellar basal-body M-ring protein (fliF)	4-17,22-44,53-60,66-83,87-94,101-106,110-116,131-137,148-183,189-207,209-215,233-242,251-262,264-272,290-296,308-327,359-373,375-380,397-405,415-420,426-433,444-475,478-484,529-536,548-558	G: 9, I: 1	106-126	35, 213
HP0380	glutamate dehydrogenase (gdhA)	4-38,42-50,58-64,72-81,92-118,140-146,157-165,172-192,198-204,208-216,227-234,238-258,271-278,288-293,311-322,327-346,357-370,375-383,395-409,411-417,425-432,436-445	H: 6, I: 1, L: 4	109-129, 370-380	36, 214
HP0392	histidine kinase (cheA)	23-30,36-49,52-64,86-94,97-104,121-129,257-272,279-286,288-294,307-327,334-340,369-375,377-386,406-412,418-423,430-438,441-447,459-465,469-476,482-488,510-546,550-580,584-622,638-645,653-659,675-683,692-705,723-731,752-761,788-795	B: 1, F: 2	54-72	37, 215
HP0401	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)	11-33,36-46,88-104,116-126,134-170,189-195,199-217,225-250,255-261,266-273,280-291,296-313,334-341,343-349,354-360,362-369,373-380,387-401,406-420	E: 1, M: 12	259-273	38, 216
HP0406	hypothetical protein	9-14,28-44,57-64,72-79,86-93,104-111,116-126,142-150,159-164	M: 2	61-86	39, 217
HP0409	GMP synthase (guaA)	10-17,26-33,43-61,69-95,101-107,109-125,129-135,137-144,147-153,158-169,177-187,209-219,221-232,235-247,261-268,271-282,296-302,306-347,355-362,364-379,386-399,409-418,424-442,451-460,467-479,490-498	B: 1, F: 1	60-74	40, 218
HP0413	transposase-like protein, PS3IS	8-14,20-31,65-84,94-99,154-179,193-207,238-253	E: 9, F: 1, G: 1	96-118	41, 219
HP0459	virB4 homolog (virB4)	4-24,30-44,47-62,84-93,108-116,124-133,136-141,201-209,217-223,228-235,238-245,247-270,275-285,290-314,328-338,342-349,353-365,375-383,386-392,394-402,417-427,443-459,465-481,492-514,516-	M: 6	167-189	42, 220

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		524,550-566,602-617,630-639,666-676,687-693,719-730,747-753,783-790,799-816,824-831,837-842			
HP0480	GTP-binding protein, fusA-homolog (yihK)	6-15,18-28,58-66,84-101,106-129,136-151,154-165,182-203,205-211,214-220,222-228,233-240,251-260,270-277,284-291,306-315,322-328,363-369,378-388,392-405,443-452,495-501,512-523,574-583	H: 1	362-375	43, 221
HP0485	catalase-like protein	5-25,27-34,47-59,64-70,76-86,145-158,166-183,189-202,217-231,235-242,260-270,278-309	A: 1, B: 2, C: 3, K: 2	1-102	44, 222
HP0508	hypothetical protein	4-19,24-76,78-83,90-99,102-109,114-122,137-147,154-174,177-188,203-212,217-223,227-239	A: 1	226-325	45, 223
HP0519	conserved hypothetical protein	7-37,71-90,94-109,117-128,141-153,179-192,199-206,225-231,237-243,258-264	B: 2, H: 1	40-51	46, 224
HP0525	virB11 homolog	13-19,25-30,46-59,75-91,101-107,114-124,129-135,137-145,160-167,171-179,187-194,209-215,217-222,229-239,243-249,257-265,269-275,299-308,310-327	D: 5	282-300	47, 225
HP0527	cag pathogenicity island protein (cag7-cagY)	86-100,216-230,342-369,382-388,424-430,438-445,452-458,488-494,501-518,554-560,568-574,584-592,603-609,611-629,639-645,652-661,669-699,708-714,726-738,747-753,763-775,785-791,794-807,815-824,826-845,854-860,863-868,870-883,892-898,901-906,909-921,930-937,946-959,968-974,977-990,998-1007,1009-1027,1037-1043,1046-1051,1053-1066,1075-1081,1084-1089,1092-1103,1113-1119,1122-1135,1143-1152,1154-1172,1182-1188,1191-1196,1200-1210,1220-1226,1229-1235,1237-1249,1259-1265,1268-1281,1289-1298,1305-1318,1328-1334,1337-1343,1345-1357,1367-1373,1390-1396,1405-1411,1418-1423,1426-1435,1445-1455,1474-1483,1493-1500,1505-1512,1517-1524,1538-1544,1568-1578,1595-1601,1674-1682,1687-1720,1728-1736,1738-1744,1754-1761,1764-1774,1798-1824,1836-1842,1886-1893,1895-1903	A: 316, B: 88, C: 61, F: 12, G: 1, H: 1, I: 7, J: 274, K: 93, L: 14, M: 12	366-781, 782-1518, 1731-1747	48, 226
HP0540	cag pathogenicity island protein (cag19)	4-17,20-39,46-55,60-66,102-110,114-122,125-131,161-167,172-178,185-190,195-202,218-232,236-252,264-291,293-302,309-315,324-339	A: 2, B: 6, C: 2, I: 1	169-381	49, 227
HP0541	cag pathogenicity	5-10,13-40,42-53,69-75,83-89,120-135,150-161,174-	B: 2, G: 1	30-200	50, 228

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	island protein (cag20)	190,203-225,229-247,257-287,318-348			
HP0542	cag pathogenicity island protein (cag21-cagG)	7-19,43-53,64-72,124-139	B: 2, L: 18, M: 2	52-84, 120-131	51, 229
HP0544	cag pathogenicity island protein (cag23-cagE)	12-19,39-48,58-100,117-123,154-162,164-187,189-195,202-216,218-235,241-246,262-278,315-328,333-347,354-366,372-379,391-405,422-429,431-442,444-450,458-466,478-485,494-501,504-510,520-535,573-580,589-598,615-625,666-676,686-698,722-729,737-746,756-767,787-796,805-816,824-829,833-848,856-864,866-876,879-886,898-904,918-924,927-934,941-960,967-978	H: 1	561-575	52, 230
HP0545	cag pathogenicity island protein (cag24)	11-29,49-55,70-77,84-100,102-112,148-155,160-177,181-204	A: 1, B: 3, I: 2, K: 1	1-104	53, 231
HP547	cag pathogenicity island protein (cag26-cagA)	27-44,64-71,122-133,151-156,164-178,214-220,226-232,235-244,253-262,282-288,294-310,317-325,350-356,362-368,376-383,438-443,449-454,459-464,492-498,500-511,529-535,538-546,567-573,597-603,660-665,674-679,724-734,763-769,773-784,791-801,807-815,821-826,840-848,863-868,897-902,908-928,932-953,956-975,980-987,990-996,1012-1018,1042-1063,1095-1116,1149-1157,1160-1167	A: 72, B: 65, C: 175, D: 74, F: 51, G: 7, H: 10, I: 108, J: 9, K: 23, L: 33, M: 129	110-357, 358-501, 502-1161	54,232
HP0563	hypothetical protein	4-21,64-71,73-84,128-138,144-162,203-217,240-263,288-298,300-308,310-317,325-351,369-380,391-411	L: 134	330-345	55, 233
HP0604	uroporphyrinogen decarboxylase (hemE)	5-11,25-31,39-48,51-79,89-98,100-122,135-148,166-201,203-227,230-250,254-260,266-272,274-282,299-305,328-337	A: 2, B: 1, F: 1, K: 2	31-45	56, 234
HP0607	acriflavine resistance protein (acrB)	12-23,29-48,51-60,66-72,75-81,83-93,103-115,133-148,168-174,195-204,222-229,231-240,242-251,270-280,286-305,322-344,349-360,364-370,378-400,421-441,448-484,486-493,495-501,504-534,547-561,567-590,597-607,621-635,643-649,658-685,688-694,702-711,717-731,737-742,759-765,767-772,776-786,803-809,815-825,854-908,910-919,923-930,942-948,961-	F: 2, G: 1, I: 1, L: 2	915-940	57, 235

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		975,994-1014			
HP0630	modulator of drug activity (mda66)	4-9,32-47,51-61,75-96,139-191	A: 1, F: 1, H: 2, I: 1	1-124	58, 236
HP0635	hypothetical protein	4-13,17-38,43-49,55-76,88-95,110-121,128-146,151-157,162-214,222-240,243-249,251-273,275-281,292-298,300-309,312-320,322-331,355-369,376-408,446-460,471-482,485-509	F: 2, H: 1	191-203	59, 237
HP0655	protective surface antigen D15	4-21,72-82,89-103,106-115,118-124,140-146,174-184,191-200,204-213,218-224,261-266,282-293,299-309,311-340,342-358,362-372,381-389,391-402,413-421,438-447,457-464,470-478,501-507,545-560,578-624,631-641,658-670,680-689,717-738,753-759,795-805,816-822,830-838,842-848,869-881,892-898	G: 1, H: 2	33-51, 818-835	60, 238
HP0659	hypothetical protein	4-21,79-85,156-177,183-188,206-214,243-249,261-269,287-292,315-322,334-345,360-366,374-390,402-411	A: 4, B: 1, K: 2	37-97, 260-399	61, 239
HP0683	UDP-N-acetylglucosamine pyrophosphorylase (glmU)	4-9,19-54,58-78,97-104,111-120,126-134,137-145,163-173,178-188,193-203,211-224,246-286,288-324,337-346,355-362,374-390,392-398,409-417	G:8	240-249	62, 240
HP0687	iron(II) transport protein (feoB)	5-12,14-31,35-41,43-61,82-92,97-105,134-145,155-166,184-203,215-223,225-251,272-279,281-306,310-345,358-418,435-473,482-490,525-532,538-547,549-563,578-604,613-639	F: 1, L: 3	144-154	63, 241
HP0696	N-methylhydantoinase	53-59,64-72,74-100,133-152,154-172,176-181,207-214,225-238,275-297,304-310,331-340,362-367,384-395,403-410,437-443,448-456,482-490,579-597,602-610,625-630,633-651,699-707,709-715,734-743,750-762	A: 5, B: 6, C: 13, E: 2, F: 1, G: 1, L: 1	544-685	64, 242
HP0701	DNA gyrase, sub A (gyrA)	12-18,22-40,45-83,89-97,103-109,147-153,159-173,195-204,210-219,243-253,259-265,273-282,303-309,315-325,332-340,346-358,362-367,377-390,393-402,418-426,447-455,467-480,505-512,514-525,548-561,566-576,584-596,619-626,638-645,649-659,661-680,699-708,714-720,753-759,766-772,775-781,801-808	G: 2, H: 2, I: 3, L: 1	202-218, 282-299, 339-350, 617-628	65, 243
HP0706	outer membrane protein (omp15)	5-33,52-62,87-101,111-135,137-143,145-152,190-202,209-221,233-245,253-270	J: 1, K: 1, L: 37	151-215	66, 244

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP0714	RNA polymerase sigma-54 factor (rpoN)	19-29,32-39,42-48,75-94,124-135,137-145,152-160,176-182,193-203,215-236,266-273,275-291,297-306,311-319,322-342,348-360,369-378,394-401	F : 7	48-64	67, 245
HP0717	DNA polymerase III gamma and tau subunits (dnaX)	4-11,13-33,36-43,53-63,65-80,112-129,134-141,143-155,157-168,178-188,191-199,201-207,215-229,242-255,263-270,283-315,320-329,333-338,340-349,412-426,465-478,485-490,498-512,540-554	A: 2, B: 3, M: 2	390-516	68,246
HP0723	L-asparaginase II (ansB)	4-18,23-32,41-47,54-70,88-99,104-111,118-138,143-148,150-162,168-175,181-188,203-211,214-220,227-245,251-268,275-281,287-296,323-333	B: 1, F: 1, H: 6, K: 2	1-90	69, 247
HP0727	transcriptional regulator, putative	8-34,38-49,72-83,85-91,94-104,112-125,134-142,148-168,181-189,191-198,202-214,222-233,242-254,256-262,273-278,287-294,314-325	B: 2, G: 2, I: 2	141-159	70, 248
HP0752	flagellar hook-associated protein 2 (fliD)	4-24,30-36,47-75,82-105,124-134,151-157,192-202,208-214,219-226,234-247,285-290,318-324,332-340,343-349,380-386,453-462,472-478,484-501,531-540,550-557,604-612,620-625,642-648,652-671	A:7, B:4, C:2, G:1, H:1, I:3, J:1, K:2	64-84, 93-180, 181-446	71, 249
HP0760	conserved hypothetical protein	12-18,24-32,68-75,77-83,96-101,109-116,129-136,152-164,175-184,190-199,206-215,224-233,241-250,258-264,273-292,302-312,319-331,334-346,348-368,387-395,408-416,420-429,437-452	F: 3, G: 1	364-374	72, 250
HP0836	hypothetical protein	11-28,36-52,60-67,74-79,108-116	B: 1, L: 4	61-76	73, 251
HP0850	type I restriction enzyme M protein (hsdM)	20-27,38-49,69-74,84-107,138-145,161-168,179-195,210-226,228-252,267-281,283-296,305-311,333-340,342-356,361-372,380-399,401-414,458-466,475-481,492-507,515-520	H: 2	146-160	74, 252
HP0853	ABC transporter, ATP-binding protein (yheS)	43-61,68-74,76-90,120-128,130-149,156-161,164-182,206-234,242-252,269-274,291-304,332-345,349-355,360-371,374-388,434-440,447-453,459-465,469-496,504-522	M: 15	261-285	75, 253
HP0863	hypothetical protein	4-17,24-30,37-49,87-98,118-124,126-136,144-171,176-188,206-214,216-228,233-240,246-252,262-271,277-297,307-330,333-342,346-352,355-361,368-386,391-400,413-420,474-480	E: 1, M: 11	401-427	76, 254
HP0874	hypothetical protein	15-26,31-46,51-72,80-93,96-109,131-137,150-158,179-185,189-209,211-219,221-234,241-247,255-262,265-271,283-288	F: 2	173-190	77, 255
HP0875	catalase	28-37,39-45,51-58,77-84,89-97,132-148,171-	K: 6	425-497	78, 256

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		180,199-205,212-218,220-226,257-265,273-300,307-327,334-340,344-365,385-390,402-408,426-436,450-468,476-485			
HP0876	iron-regulated outer membrane protein (frpB)	4-25,70-76,80-88,90-100,120-128,162-169,183-203,261-277,279-289,291-297,302-308,321-327,339-353,358-377,392-401,404-410,414-422,443-450,456-461,470-488,490-497,510-535,570-611,618-630,639-647,649-660,668-690,702-716,718-724,737-747,750-764	B: 1, E: 1, G: 1, I: 1	497-509	79, 257
HP0887	vacuolating cytotoxin	12-48,50-64,99-108,216-223,235-241,244-254,262-274,287-293,310-316,320-326,361-366,377-383,390-395,408-414,418-425,438-444,462-469,494-505,524-530,536-547,551-566,592-598,601-613,678-685,687-695,709-717,727-737,751-757,760-765,772-778,782-788,801-807,822-830,859-868,870-878,884-890,898-903,909-919,953-969,973-980,990-1000,1002-1019,1041-1047,1059-1065,1090-1095,1116-1127,1130-1139,1143-1149,1151-1168,1178-1183,1188-1195,1197-1209,1213-1220,1226-1234,1236-1247,1255-1274,1276-1282	A: 1, B: 5, C: 2, D: 3, E: 5, G: 2, H: 3, I: 2, K: 9, L: 29, M: 7	76-100, 270-284, 309-438, 493- 505, 786-942, 947-967	80, 258
HP0891	conserved hypothetical protein	4-9,24-34,46-95,97-109,119-130	F: 2	138-156	81, 259
HP0910	adenine specific DNA methyltransferase (HINDIIM)	9-26,28-35,43-53,55-68,83-92,99-105,110-135,139-149,157-162,164-170,173-183,193-208,210-230,239-245,253-259,263-271,293-305,310-320,322-331,336-343,351-364,367-376	E: 33, H: 1	92-107, 154-173	82, 260
HP0913	outer membrane protein (omp21)	19-39,52-62,108-117,145-152,160-168,194-203,229-240,252-268,280-287,308-316,333-339,383-390,403-412,414-424,438-445,464-472,479-484,489-505,510-526	C: 1, I: 1	247-260	83, 261
HP0922	toxin-like outer membrane protein	5-17,25-52,60-77,105-113,118-125,162-167,228-234,272-279,328-334,341-357,381-395,400-406,512-518,557-569,586-592,645-651,690-695,701-709,720-726,733-743,751-758,781-786,879-886,929-934,939-944,952-960,965-975,994-1001,1039-1045,1102-1109,1164-1181,1198-1206,1223-1229,1253-1259,1283-1292,1312-1317,1339-1349,1360-1370,1389-1398,1400-1412,1452-1465,1470-	A: 1, B: 3, D: 1, F: 4, G: 2	394-549	84, 262

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		1484,1490-1497,1519-1525,1554-1564,1578-1591,1623-1636,1638-1646,1669-1679,1685-1697,1704-1711,1713-1720,1730-1736,1738-1749,1756-1764,1778-1786,1796-1803,1817-1826,1849-1866,1975-1993,2017-2032,2044-2053,2070-2086,2091-2109,2116-2127,2156-2167,2182-2188,2197-2202,2244-2252,2281-2287,2290-2307,2350-2361,2383-2404,2425-2433,2445-2455,2495-2505			
HP0925	recombinational DNA repair protein (recR)	9-24,31-53,57-67,69-79,84-114,133-141,144-172,178-186	E: 1, G: 1	13-46	85, 263
HP0953	hypothetical protein	4-25,27-35,43-52,59-70,79-91,115-130,136-152,154-163,170-179	J: 3	1-58	86, 264
HP0973	hypothetical protein	4-30,49-55,71-80,96-105,111-126,139-146,149-162,239-245,279-285,290-296,300-307,331-337,343-350	B: 3, K: 2	250-351	87, 265
HP0977	conserved hypothetical secreted protein	9-27,34-41,43-51,92-111,114-120,123-131,139-150,156-171,176-186,188-204,229-241,252-258,266-279,288-297,319-334,338-348,373-379,389-398,431-439,479-484	A: 2	214-398	88, 266
HP1019	serine protease (htrA)	4-15,18-27,47-52,68-83,91-97,104-110,115-121,139-147,157-164,198-206,227-236,241-254,264-273,278-289,311-320,353-361,372-383,405-420,426-434	A: 3, H: 1, I: 1	232-386	89, 267
HP1024	co-chaperone-curved DNA binding protein A (CbpA)	4-10,24-34,91-97,129-141,156-163,184-190,205-219,229-235,256-273,278-285	E: 1, G: 1, L: 24	93-116	90, 268
HP1052	UDP-3-0-acyl N-acetylglcosamine deacetylase (envA)	7-29,35-54,71-83,85-91,104-111,122-134,138-144,146-154,158-174,177-183,186-201,207-215,223-235,240-247,262-273,275-283,287-292	E: 1, F: 5, G: 14	48-66	91, 269
HP1090	cell division protein (ftsK)	7-27,31-47,49-70,75-102,110-149,157-171,217-223,235-251,294-302,358-364,367-375,387-393,395-412,423-430,441-451,456-470,472-486,488-495,499-509,515-529,536-549,556-570,574-603,607-615,625-633,642-658,670-676,683-702,708-716,720-726,747-756,763-784,803-812,815-826	D: 2, F: 1, G: 1, H: 1	475-490	92, 270
HP1098	conserved	7-22,30-38,53-59,64-75,83-95,97-112,120-131,133-	A: 4, B: 1,	9-156, 174-287	93, 271

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	hypothetical secreted protein	142,145-151,154-166,172-180,189-203,227-238,277-287	F: 1, I: 2, K: 1		
HP1116	hypothetical protein	13-23,25-32,111-117,150-164,185-193,207-212,216-224,230-236,263-272,304-311,342-348,374-385,391-407,444-458,480-487,489-499,523-542,544-558,572-579,620-640,686-696,703-710,742-755,765-772,817-822,830-837,865-872,931-937	I: 1, K: 2, L: 31	66-86	94, 272
HP1117	conserved hypothetical secreted protein	4-27,49-56,62-70,86-92,121-127,151-163,170-182,195-202,212-226,237-243	A: 1, F: 4	234-254	95, 273
HP1119	flagellar hook-associated protein 1 (HAP1) (flgK)	4-10,13-24,39-51,62-78,92-104,107-117,134-141,156-161,166-181,210-216,222-229,256-266,273-280,297-304,313-330,336-349,371-376,433-439,443-448,488-493,506-515,527-534,560-572,575-583,587-593	A: 7, B: 1, D: 1, F: 3, J: 1	252-483	96, 274
HP1126	colicin tolerance-like protein (tolB)	4-15,21-38,45-56,81-95,102-108,118-130,133-147,152-162,166-171,199-204,211-218,230-240,253-261,274-283,288-294,312-317,325-336,344-357,391-414	A: 3, B: 2, J: 1	24-146	97, 275
HP1152	signal recognition particle protein (ffh)	26-31,38-56,65-82,90-101,112-119,123-153,175-188,197-216,234-242,249-265,273-286,290-305,327-335,338-346,361-372,394-404	D : 1, F : 4, G : 10	290-306	98, 276
HP1153	valyl-tRNA synthetase (valS)	17-26,43-48,50-73,81-93,95-107,139-146,158-168,171-176,190-196,202-212,216-223,243-266,274-282,308-313,324-330,344-378,380-387,403-422,427-443,448-455,457-465,491-515,517-528,553-567,589-599,610-617,642-648,670-697,709-717,726-743,745-759,769-803,807-823,840-849	F: 4, G: 3, L: 3	820-851	99, 277
HP1186	carbonic anhydrase	4-18,39-48,53-63,66-90,102-117,125-134,137-145,156-162,169-197	D: 5, H: 1	26-40, 56-80	100, 278
HP1198	DNA-directed RNA polymerase, beta subunit (rpoB)	21-33,36-42,49-60,68-76,91-105,123-130,141-161,169-178,185-190,192-199,205-214,223-233,239-247,260-269,284-293,300-314,324-352,357-364,373-382,389-403,420-432,438-446,466-471,477-484,503-509,549-556,558-576,600-623,625-635,654-661,663-669,671-687,702-716,735-741,744-750,757-766,776-786,807-815,824-832,854-860,863-897,909-915,920-946,952-959,982-997,1024-1038,1049-1055,1071-	A: 26, B: 14, C: 25, D: 3, F: 1, G: 3, I: 3, J: 31, K: 2	213-344, 954-1080, 2524-2733	101, 279

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		1085,1104-1113,1121-1132,1138-1150,1187-1196,1212-1221,1227-1236,1257-1262,1264-1278,1282-1294,1307-1318,1353-1370,1382-1388,1396-1409,1434-1440,1446-1454,1465-1478,1485-1513,1516-1529,1540-1545,1563-1568,1575-1593,1607-1616,1628-1645,1648-1661,1676-1682,1689-1697,1713-1719,1739-1749,1753-1758,1763-1774,1797-1803,1807-1846,1855-1874,1877-1891,1893-1907,1912-1925,1931-1943,1955-1965,1976-1990,2032-2043,2045-2051,2099-2105,2131-2138,2161-2179,2188-2199,2205-2216,2219-2227,2235-2245,2247-2267,2277-2288,2294-2304,2314-2326,2346-2358,2365-2377,2383-2402,2407-2423,2437-2450,2454-2473,2489-2497,2525-2531,2557-2570,2580-2587,2589-2599,2621-2641,2647-2653,2661-2677,2685-2690,2697-2717,2722-2733,2739-2777,2786-2793,2801-2808,2811-2822,2825-2835,2838-2845,2859-2871,2877-2883			
HP1205	translation elongation factor EF-Tu (tufB)	10-16,18-23,28-41,63-69,77-91,101-109,118-136,146-153,155-162,168-179,192-207,217-226,229-235,239-254,279-286,294-307,313-319,334-341,344-353,363-377,390-396	A : 4, B : 1	178-328	102, 280
HP1229	aspartokinase (lysC)	18-42,68-84,89-95,100-105,107-115,125-135,154-177,189-195,205-228,236-243,252-259,279-300,309-316,323-331,340-351,353-364,377-402	I: 1, K: 1, L: 3	85-97	103, 281
HP1243	outer membrane protein (omp28)	4-18,26-32,66-76,100-126,151-159,178-186,188-194,200-210,241-248,253-259,262-279,284-291,307-313,315-322,327-337,376-386,399-407,432-441,467-473,487-497,499-505,543-549,560-568,585-593,598-604,608-614,630-642,647-653,690-703,717-730	B: 3, F: 1, G: 1, H: 1	21-200, 468-480	104, 282
HP1254	biotin synthesis protein (bioC)	17-49,52-58,62-73,78-97,100-117,122-172,185-190,193-217,225-236	H: 2, I: 2	33-42	105, 283
HP1265	hypothetical protein	7-39,50-58,73-89,96-107,109-120,126-142,152-170,178-202,205-211,224-244,249-259,261-270,300-310,312-325	F: 2, G: 6, I: 1	158-169	106, 284
HP1282	anthranilate	4-31,40-64,71-82,85-92,102-124,126-139,147-	B: 20, G:	201-221	107,

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	synthase component I (trpE)	152,159-173,176-188,195-207,210-216,234-241,249-256,258-276,279-293,296-302,310-315,349-356,363-378,380-403,411-426,435-441,448-459,463-476,488-494	1, I: 1		285
HP1329	cation efflux system protein (czcA)	5-13,15-74,87-104,107-120,123-129,136-145,150-191,193-206,227-248,250-264,278-302,304-323,332-378,384-407,409-419,425-457,462-471,474-497,511-545,555-564,571-578,585-598,640-647,669-675,682-691,693-705,729-743,752-761,772-780,786-804,808-818,822-846,858-880,884-900,910-939,941-947,962-971,973-988,998-1003,1007-1027	B: 2, F: 1, J: 1, L: 2	236-259	108, 286
HP1339	biopolymer transport protein (exbB)	4-19,27-68,81-111,121-160	F: 5, I: 4	60-79	109, 287
HP1341	siderophore-mediated iron transport protein	4-37,40-46,52-57,199-205,222-229,236-244,250-267,269-282	A: 20, B: 23, C: 30, E: 31, F: 5, G: 3, H: 6, I: 1, J: 2, K: 5	27-197	110, 288
HP1342	outer membrane protein (omp29)	4-16, 24-30, 32-38, 63-75, 86-92, 98-111, 113-126, 160-165, 170-180, 198-204, 227-233, 239-245, 253-273, 308-314, 352-365, 382-387, 395-403, 423-429, 472-482, 484-493, 501-507, 518-526, 536-541, 543-550, 556-562, 586-600, 626-633, 649-661, 680-688	A: 1, B: 3, C: 1, D: 1, E: 1, F: 2, H: 7	546-559	111, 289
HP1345	phosphoglycerate kinase	16-33,48-59,63-71,77-92,94-109,117-124,139-151,169-181,184-227,233-249,251-261,263-275,282-294,297-321,326-332,341-355,383-399	D: 20, I: 6	258-272	112, 290
HP1350	protease	11-26,31-39,43-52,55-62,64-70,80-94,123-133,135-141,172-181,185-206,209-218,224-230,238-244,251-262,264-271,290-301,306-324,333-340,350-357,367-375,390-397,434-441,443-448	A: 3, B: 1, C: 1, G: 1, K: 2, M: 12	77-226, 350-429	113, 291
HP1374	ATP-dependent protease ATPase subunit (clpX)	4-13,22-27,31-45,50-59,72-96,99-114,131-141,143-150,159-176,180-186,189-198,208-214,234-253,271-287,294-299,310-366,382-390,398-416,424-443	G: 9, M: 2	283-305	114, 292
HP1393	DNA repair protein (recN)	9-26,30-53,62-72,86-95,112-122,136-145,153-160,209-221,227-237,241-268,281-288,291-298,308-314,321-328,336-346,351-379,388-397,409-416,423-	E: 1, F: 2, G: 7, I: 1	213-232	115, 293

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		433,443-481,511-519			
HP1448	ribonuclease P, protein component (rnpA)	12-18,25-31,38-50,59-67,71-82,96-126	G: 6	76-88	116, 294
HP1453	conserved hypothetical protein	4-25,39-44,64-71,74-88,100-113,128-138,151-162,164-177,185-190,204-213,233-239,246-254,281-286,293-306,309-318,333-347,349-359,385-398,404-423,458-465,477-484,490-499,501-533,554-566,582-590,596-616,624-629,631-639,654-680,694-720,735-743	B: 1, D: 4, F: 2, J: 1, K: 11, L: 3	2-100	117, 295
HP1454	hypothetical protein	4-16,36-41,52-75,98-107,109-117,122-128,133-139,141-155,159-165,169-182,187-193,195-201,211-224,230-236,247-269,278-290	B: 1, M: 8	75-92	118, 296
HP1460	DNA polymerase III alpha-subunit (dnaE)	7-21,25-33,37-43,87-94,103-120,131-147,168-174,197-203,207-212,227-237,247-257,263-271,279-287,298-306,320-325,332-340,363-374,379-384,390-401,403-414,428-433,448-457,462-475,483-490,513-519,525-535,543-554,559-566,571-620,625-631,636-642,659-670,688-706,708-723,770-779,787-793,796-807,820-840,848-854,863-874,895-905,912-919,934-942,968-975,983-1000,1012-1019,1026-1036,1050-1060,1064-1070,1081-1091,1094-1108,1112-1118,1140-1152,1164-1169,1172-1180,1187-1192	F: 3, G: 2, I: 3	732-748	119, 297
HP1497	peptidyl-tRNA hydrolase (pth)	23-40,42-59,66-73,78-97,111-128,130-141,157-166,178-183	E: 6, F: 1, H: 2	53-71	120, 298
HP1527	hypothetical protein	4-27,38-44,47-57,59-85,99-106,114-121,154-166,181-186,193-198,238-244,253-262,272-278,287-299,314-320,338-350,358-368,382-388,407-416,433-446,456-461,463-473	B: 3, C: 1, I: 7	86-195	121, 299
HP1564	outer membrane protein	5-24,38-59,64-80,87-99,105-126,134-142,149-163,165-179,181-202,205-220,227-233,243-250,257-263	A: 2, B: 1, C: 3, F: 1, H: 1	87-245	122, 300
HP1565	penicillin-binding protein 2 (pbp2)	5-32,47-53,66-79,81-97,115-151,155-174,183-188,196-210,215-226,230-238,253-258,263-270,276-282,295-301,304-325,334-344,360-390,397-412,425-432,434-462,478-494,508-526,539-564,571-579	A: 1, F: 2, H: 1, L: 5	347-371, 375-386	123, 301
HP1574	riboflavin synthase alpha subunit (ribC)	4-15,36-44,49-56,60-66,68-82,84-103,109-115,118-141,147-154,160-168,176-185	H: 1, M: 5	26-39	124, 302

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
ARF0044	Hypothetical protein	7-13,23-33	H: 1, I: 2	13-21	125, 303
ARF0048	Hypothetical protein	none	F: 1, G: 1, I: 4, L: 8	2-10	126, 304
ARF0143	Hypothetical protein	4-9,12-18,35-42,49-62	F: 1	6-18	127, 305
ARF0184	Hypothetical protein	19-25	A: 1, I: 6	1-13	128, 306
ARF0219	Hypothetical protein	15-21,27-45	E: 7	12-25	129, 307
ARF0308	Hypothetical protein	14-20	E: 41	1-14	130, 308
ARF0349	Hypothetical protein	4-18	G:11	13-26	131, 309
ARF0387	Hypothetical protein	8-21	G: 12, H: 2, K: 1	2-20	132, 310
ARF0402	Hypothetical protein	4-14	F: 2, G: 10, H: 1, M: 2	4-16	133, 311
ARF0501	Hypothetical protein	none	M: 2	3-12	134, 312
ARF0509	Hypothetical protein	6-14,6-25,35-57	G: 5, H: 1, M: 3	2-14	135, 313
ARF0522	Hypothetical protein	6-25,35-57	F: 1, I: 3, K: 2	17-31	136, 314
ARF0578	Hypothetical protein	14-25,32-46	E: 12, G: 1	5-19	137, 315
ARF0629	Hypothetical protein	18-31	G: 1, I: 7	5-16	138, 316
ARF0665	Hypothetical protein	19-24	L: 2, M: 5	4-26	139, 317
ARF0693	Hypothetical protein	13-21,29-34,47-58,61-73	G: 1, I: 6	36-47	140, 318
ARF0752	Hypothetical protein	4-15	D:3	5-24	141, 319
ARF0788	Hypothetical protein	none	B: 1, H: 1	6-18	142, [illegible]

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
					320
ARF0819	Hypothetical protein	13-20	F: 14	4-13	143, 321
ARF0839	Hypothetical protein	none	A: 2, C: 1, I: 1, K: 3	15-23	144, 322
ARF0868	Hypothetical protein	4-9	F: 2, G: 1	7-21	145, 323
ARF0948	Hypothetical protein	none	F: 1	1-10	146, 324
ARF0969	Hypothetical protein	none	B: 1, G: 1, M: 2	4-14	147, 325
ARF1100	Hypothetical protein	4-17,35-41,46-89,93-98	A: 1, B: 1, H: 1, I: 2, M: 5	70-88	148, 326
ARF1164	Hypothetical protein	none	G: 1, H: 3, J: 1, M: 2	1-13	149, 327
ARF1470	Hypothetical protein	4-16,26-32	G: 1, I: 1, M: 2	25-38	150, 328
ARF1553	Hypothetical protein	8-15,23-28	B: 2, F: 6, G: 2, H: 1, I: 1, K: 1	4-17	151, 329
CRF0017	Hypothetical protein	4-12	H: 1, I: 1, M: 5	1-15	152, 330
CRF0025	Hypothetical protein	4-29,31-42,52-58	E: 1, G: 1, L: 3, M: 1	6-16	153, 331
CRF0090	Hypothetical protein	4-9,24-32	F: 13, G: 1, H: 1, L: 1	9-19	154, 332
CRF0127	Hypothetical protein	4-12,18-27	L: 3, M: 10	5-18	155, 333
CRF0169	Hypothetical protein	4-11,37-56,58-92	D: 3	18-29	156, 334
CRF0190	Hypothetical protein	8-28	M: 14	20-35	157, 335
CRF0251	Hypothetical protein	none	D: 16, E: 2, G: 3	4-15	158, 336
CRF0258	Hypothetical protein	4-23,27-39,55-63	A: 1, B: 1, [illegible]	35-58	159, [illegible]

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
			C: 1, F: 1, L: 5		337
CRF0354	Hypothetical protein	6-26,28-54	F: 8, H: 1	28-47	160, 338
CRF0388	Hypothetical protein	4-10,38-52,58-82	H: 1, L: 3	30-49	161, 339
CRF0409	Hypothetical protein	4-22,29-35,44-50,53-68,70-80	G: 2, H: 1, M: 10	20-33	162, 340
CRF0421	Hypothetical protein	22-28,30-36	F: 4	18-33	163, 341
CRF0480	Hypothetical protein	4-11,13-21,25-30	E: 1, L: 8	20-30	164, 342
CRF0552	Hypothetical protein	10-22	G: 1, M: 5	10-23	165, 343
CRF0563	Hypothetical protein	4-11	G: 1, L: 1, M: 6	9-20	166, 344
CRF0578	Hypothetical protein	14-25,32-46	G: 1, L: 7, M: 12	6-19	167, 345
CRF0626	Hypothetical protein	5-30	L: 43	14-33	168, 346
CRF0870	Hypothetical protein	4-15,28-35,46-55,59-65,76-84	H: 6, I: 1, L: 8	9-24	169, 347
CRF0894	Hypothetical protein	27-33	L: 5	5-19	170, 348
CRF0922	Hypothetical protein	5-13	E: 11, F: 3, G: 1, H: 7, I: 1, L: 4	8-18	171, 349
CRF1012	Hypothetical protein	9-22,24-34	L: 3	21-40	172, 350
CRF1100	Hypothetical protein	4-17,35-41,46-89,93-98	E: 1, H: 5, I: 2, L: 4	71-89	173, 351
CRF1301	Hypothetical protein	4-12,14-24	H: 9, I: 2	2-17	174, 352
CRF1354	Hypothetical protein	9-17	I: 2, M: 16	5-16	175, 353
CRF1422	Hypothetical protein	7-41,48-58,63-75,80-89	G: 2, H: 1, [illegible]	43-53	176, [illegible]

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
			L: 62		354
CRF1489	Hypothetical protein	4-22,25-30	E: 1, F: 1, H: 5, L: 10	4-14	177, 355
CRF1549	Hypothetical protein	4-55	G: 1, M: 7	18-33	178, 356

Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence which is selected from the group consisting of:
   a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from Seq ID No 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178,
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.

3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from Seq ID No 8-10, 13-15, 17-18, 24, 27, 32, 39-40, 45-47, 56, 59, 62, 69-70, 73, 77, 79, 82, 85-86, 88, 90, 103, 109-110, 114, 121.
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

4. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule selected from Seq ID No 5, 7, 30-31, 53, 60, 66, 76, 83, 87, 92, 99, 120,
   b) a nucleic acid molecule which is complementary to the nucleic acid of a),
   c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

5. The nucleic acid molecule according to any one of the claims 1, 2, 3 or 4, wherein the nucleic acid is DNA.

6. The nucleic acid molecule according to any one of the claims 1,2, 3, 4, or 5 wherein the nucleic acid is RNA.

7. An isolated nucleic acid molecule according to any one of claims 1 to 5, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a *H. pylori* genomic DNA.

8. A vector comprising a nucleic acid molecule according to any one of claims 1 to 7.

9. A vector according to claim 8, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 7.

10. A host cell comprising the vector according to claim 8 or 9.

11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 5, 6 or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 181-182, 194, 197-199, 206-207, 211-216, 219-220, 222, 226-230, 233, 235-236, 239, 241, 243, 245-246, 250, 252-253, 259, 262, 269, 272, 274-275, 279, 283-286, 290, 293-295, 297, 301-356.

12. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 3, 5, 6, or 7 and fragments thereof, wherein the amino acid sueqnece is selected from the group consisting of Seq ID No 186-188, 191-193, 195-196, 202, 205, 210, 217-218, 223-225, 234, 237, 240, 247-248, 251, 255, 257, 260, 263-264, 266, 268, 281, 287-288, 292, 299.

13. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 4, 5, 6, or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 183, 185, 208-209, 231, 238, 244, 254, 261, 265, 270, 277, 298.

14. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1, especially peptides comprising amino acid 63-91, 95-101, 110-116, 134-148, 150-156, 158-164, 188-193, 197-209, 226-241, 247-254, 291-297, 312-319, 338-346, 351-358, 366-378, 404-410, 420-438, 448-454, 465-473, 482-488, 490-498, 503-510, 512-519, 531-543, 547-554, 568-575, 589-604, 610-631 and 239-308 of Seq ID No 179; 16-29, 35-47, 50-68, 70-79, 91-101, 143-149, 158-163, 185-191, 196-206, 215-224, 230-237, 244-251, 258-278, 290-311, 319-325, 338-351, 365-385, 396-429, 445-454, 458-466, 491-499, 501-521, 17-79 and 218-233 of Seq ID No 180; 4-10, 16-41, 46-66, 77-84, 91-97, 102-118, 125-144, 187-200, 202-214, 245-253, 255-261, 286-295, 300-330, 335-342, 350-361, 363-381, 385-392, 396-416, 435-450 and 460-470 of Seq ID No 181; 11-19, 27-48, 52-59, 77-82, 84-107, 118-125, 127-154, 178-183, 192-209, 215-221, 286-295, 302-313, 350-357, 402-415, 417-431, 453-463, 465-493 and 313-331 of Seq ID No 182; 19-26, 30-43, 47-55, 63-68, 72-80, 97-104, 107-119, 129-146, 160-175, 194-216, 231-251, 254-260 and 26-43 of Seq ID No 183; 7-13, 29-37, 65-81, 110-120, 123-131, 135-152, 230-249, 254-260, 284-290, 292-299, 317-326, 329-336, 403-444, 452-458, 466-477, 490-498, 510-519, 541-550, 557-566 and 533-567 of Seq ID No 184; 5-47, 71-77, 79-86, 89-95, 120-126, 137-144, 176-181, 184-196, 202-208, 211-232, 236-282, 301-313, 317-325, 341-347, 353-384, 394-400, 412-433, 436-443 and 59-75 of Seq ID No 185; 4-18, 22-38, 59-69, 106-112, 116-130, 138-149, 156-170, 175-197, 200-214, 216-223, 233-244, 255-261, 266-276, 279-286, 325-333, 342-348, 366-399, 402-420, 429-441, 1-104 and 130-147 of Seq ID No 186; 50-58, 69-95, 97-113, 131-136, 157-163, 170-175, 188-212, 220-226, 254-259, 265-277, 283-289, 297-308, 311-318, 347-358, 360-369, 378-401, 416-421, 440-450, 454-462, 470-476, 493-502, 506-514, 536-567, 585-590, 598-607, 613-618, 653-659 and 35-46 of Seq ID No 187; 16-29, 32-60, 65-87, 89-123, 128-134, 137-158, 162-173, 178-196, 210-216, 218-228 and 206-225 of Seq ID No 188; 10-20, 26-35, 51-64, 86-91, 94-100, 113-122, 154-160, 185-191, 193-201, 211-217, 225-230, 237-246, 251-257, 298-304, 306-312, 316-328, 340-348, 357-389, 391-397, 415-421, 449-456, 458-471, 488-495, 502-511, 24-55 and 236-341 of Seq ID No 189; 5-22, 41-51, 87-93, 114-122, 127-136, 150-156, 158-166, 223-233, 245-263, 291-296, 9-126 and 127-285 of Seq ID No 190; 30-43, 46-56, 61-70, 72-83, 85-93, 103-113, 119-125, 151-166, 179-191, 212-218, 225-231, 236-243, 262-267, 291-307, 331-344, 349-355, 366-372, 380-386, 414-422, 428-447, 459-464, 469-478, 507-519, 525-544, 563-569, 576-590, 620-626, 633-643, 654-659, 665-671, 684-707, 717-723, 725-733, 747-779, 782-801 and 347-361 of Seq ID No 191; 4-12, 14-26, 37-80, 107-115, 133-139, 144-150, 154-165, 173-180, 191-199, 205-211, 221-231, 237-244, 254-284, 307-340, 342-353, 360-368, 370-380, 479-493, 495-503, 509-522, 525-536, 539-547, 554-560,

565-573, 578-583, 7-23 and 465-479 of Seq ID No 192; 4-17, 47-55, 76-83, 85-100, 104-112, 117-123, 126-135, 142-148, 156-167, 174-182, 267-273 and 258-283 of Seq ID No 193; 8-32, 36-42, 65-88, 102-108, 112-140, 147-163, 170-179, 183-193 and 117-124 of Seq ID No 194; 12-18, 45-50, 62-77, 82-95, 99-113, 115-123, 125-147, 155-177, 187-209, 211-223, 244-253, 259-270, 278-297, 302-307, 311-318, 329-334, 350-356, 359-365, 390-400, 402-413 and 333-350 of Seq ID No 195; 4-13, 15-27, 30-46, 53-58, 68-74, 82-95, 115-126, 134-139, 148-153, 159-176, 182-199, 201-217, 220-225, 227-235, 237-248, 253-266, 300-315, 322-336, 390-396, 412-426, 438-445, 448-459, 477-484, 502-508, 515-527, 529-537, 553-568, 643-651, 658-667, 690-703 and 376-400 of Seq ID No 196; 4-10, 24-32, 38-55, 59-67, 70-77, 80-87, 89-97, 123-129, 134-151, 166-172, 178-189, 191-216, 218-235, 245-259, 271-315, 326-339, 341-360 and 73-94 of Seq ID No 197; 13-25, 31-38, 43-57, 79-85, 92-99, 106-112, 117-128, 130-139, 146-158, 160-175, 194-204, 211-222, 225-232, 234-242, 263-270, 278-292, 299-320, 322-333 and 240-256 of Seq ID No 198; 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ID No 319; 6-18 of Seq ID No 320; 13-20 and 4-13 of Seq ID No 321; 15-23 of Seq ID No 322; 4-9 and 7-21 of Seq ID No 323; 1-10 of Seq ID No 324; 4-14 of Seq ID No 325; 4-17, 35-41, 46-89, 93-98 and 70-88 of Seq ID No 326; 1-13 of Seq ID No 327; 4-16, 26-32 and 25-38 of Seq ID No 328; 8-15, 23-28 and 4-17 of Seq ID No 329; 4-12 and 1-15 of Seq ID No 330; 4-29, 31-42, 52-58 and 6-16 of Seq ID No 331; 4-9, 24-32 and 9-19 of Seq ID No 332; 4-12, 18-27 and 5-18 of Seq ID No 333; 4-11, 37-56, 58-92 and 18-29 of Seq ID No 334; 8-28 and 20-35 of Seq ID No 335; 4-15 of Seq ID No 336; 4-23, 27-39, 55-63 and 35-58 of Seq ID No 337; 6-26, 28-54 and 28-47 of Seq ID No 338; 4-10, 38-52, 58-82 and 30-49 of Seq ID No 339; 4-22, 29-35, 44-50, 53-68, 70-80 and 20-33 of Seq ID No 340; 22-28, 30-36 and 18-33 of Seq ID No 341; 4-11, 13-21, 25-30 and 20-30 of Seq ID No 342; 10-22 and 10-23 of Seq ID No 343; 4-11 and 9-20 of Seq ID No 344; 14-25, 32-46 and 6-19 of Seq ID No 345; 5-30 and 14-33 of Seq ID No 346; 4-15, 28-35, 46-55, 59-65, 76-84 and 9-24 of Seq ID No 347; 27-33 and 5-19 of Seq ID No 348; 5-13 and 8-18 of Seq ID No 349; 9-22, 24-34 and 21-40 of Seq ID No 350; 4-17, 35-41, 46-89, 93-98 and 71-89 of Seq ID No 351; 4-12, 14-24 and 2-17 of Seq ID No 352; 9-17 and 5-16 of Seq ID No 353; 7-41, 48-58, 63-75, 80-89 and 43-53 of Seq ID No 354; 4-22, 25-30 and 4-14 of Seq ID No 355; 4-55 and 18-33 of Seq ID No 356.

15. A process for producing a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising expressing the nucleic acid molecule according to any one of claims 1 to 7.

16. A process for producing a cell, which expresses a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising transforming or transfecting a suitable host cell with the vector according to claim 8 or claim 9.

17. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of claims 11 to 14 or a nucleic acid molecule according to any one of claims 1 to 7.

18. A pharmaceutical composition, especially a vaccine, according to claim 17, characterized in that it further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

19. Use of a nucleic acid molecule according to any one of claims 1 to 7 or a hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *H. pylori* infection.

20. An antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

21. An antibody according to claim 20, wherein the antibody is a monoclonal antibody.

22. An antibody according to claim 20 or 21, wherein said effective part comprises Fab fragments.

23. An antibody according to any one of claims 20 to 22, wherein the antibody is a chimeric antibody.

24. An antibody according to any one of claims 20 to 23, wherein the antibody is a humanized antibody.

25. A hybridoma cell line, which produces an antibody according to any one of claims 20 to 24.

26. A method for producing an antibody according to claim 20, characterized by the following steps:
  - initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 11 to 14, to said animal,
  - removing an antibody containing body fluid from said animal, and
  - producing the antibody by subjecting said antibody containing body fluid to further purification steps.

27. Method for producing an antibody according to claim 21, characterized by the following steps:
  - initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 12 to 15, to said animal,
  - removing the spleen or spleen cells from said animal,
  - producing hybridoma cells of said spleen or spleen cells,
  - selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
  - producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

28. Use of the antibodies according to any one of claims 20 to 24 for the preparation of a medicament for treating or preventing *H. pylori* infections.

29. An antagonist which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

30. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 comprising:
  a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
  b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

31. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 to its interaction partner comprising:
  a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 11-14,
  b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 20 to 24,
  c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form a interaction complex,
  d) providing a candidate antagonist,
  e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex ,

f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

32. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

33. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11-14.

34. A process for *in vitro* diagnosis of a bacterial infection, especially a *H. pylori* infection, comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14.

35. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalines.

36. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

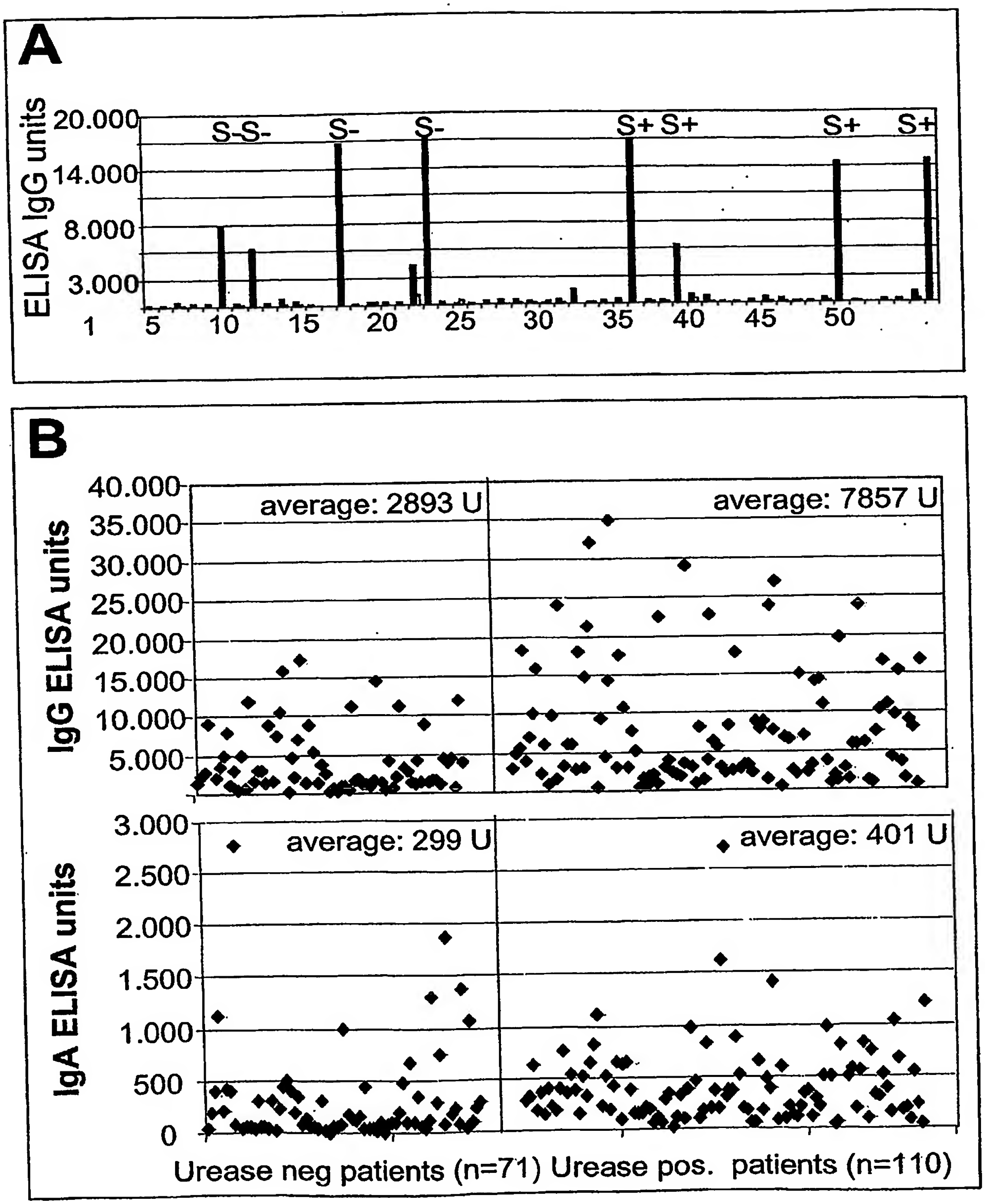
37. Use of a nucleic acid molecule according to any one of claims 11 to 14 for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

Summary:

H. pylori antigens

The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *H. pylori*, methods for isolating such antigens and specific uses thereof.

[no Fig. on front page]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average: 7857 U
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Figure 1

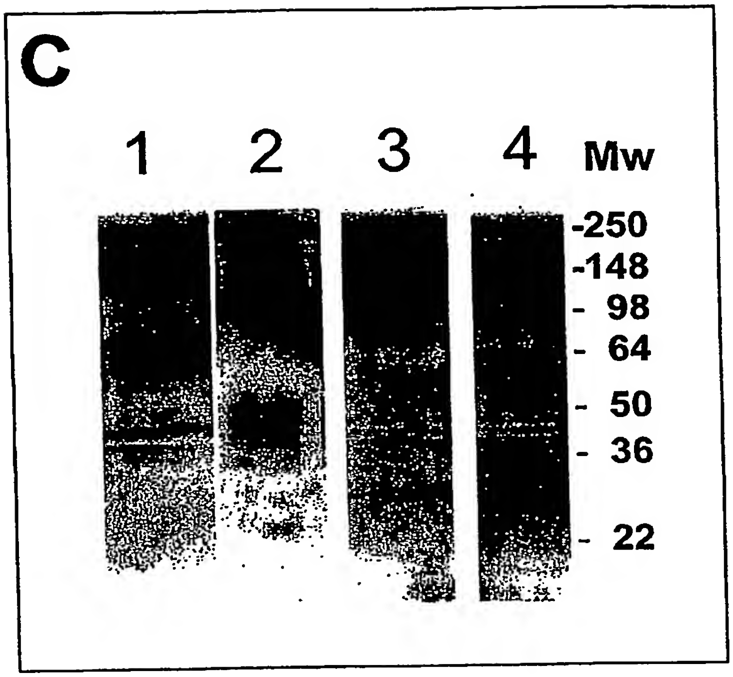
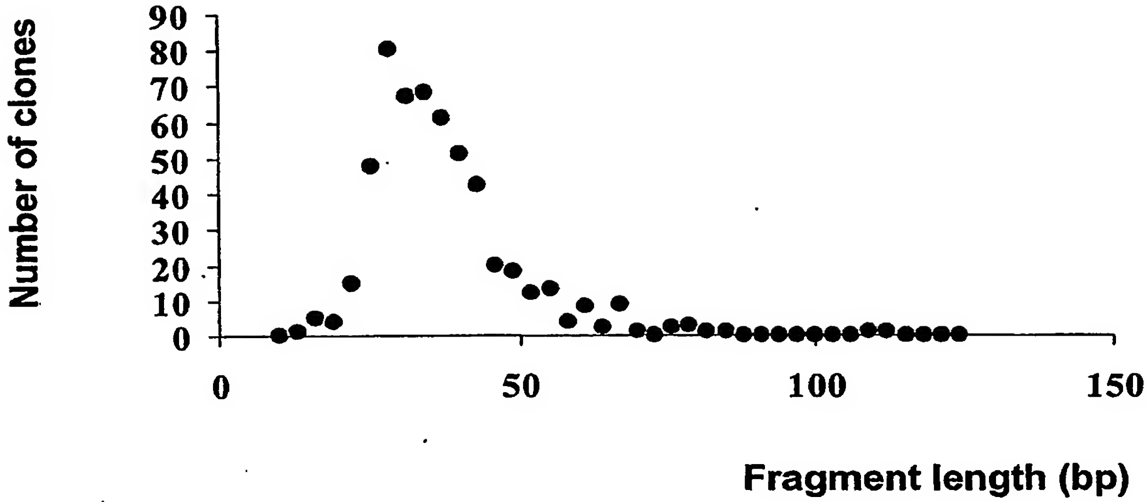


Fig. 1

A.



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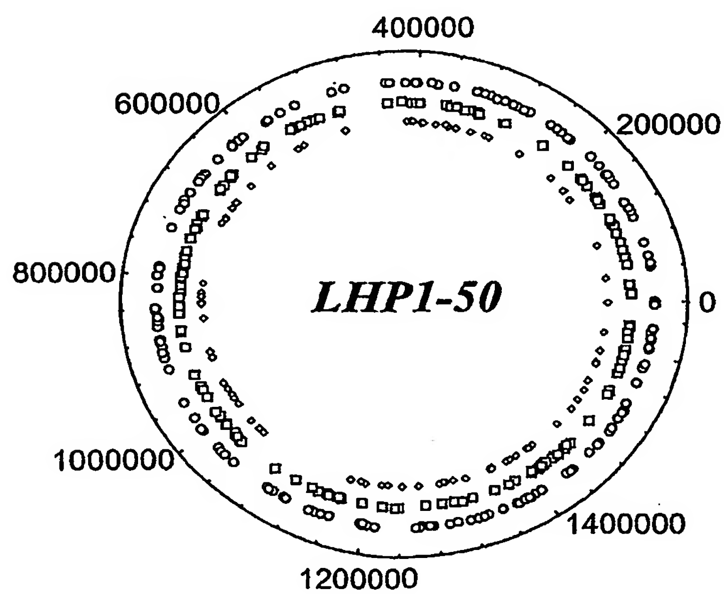
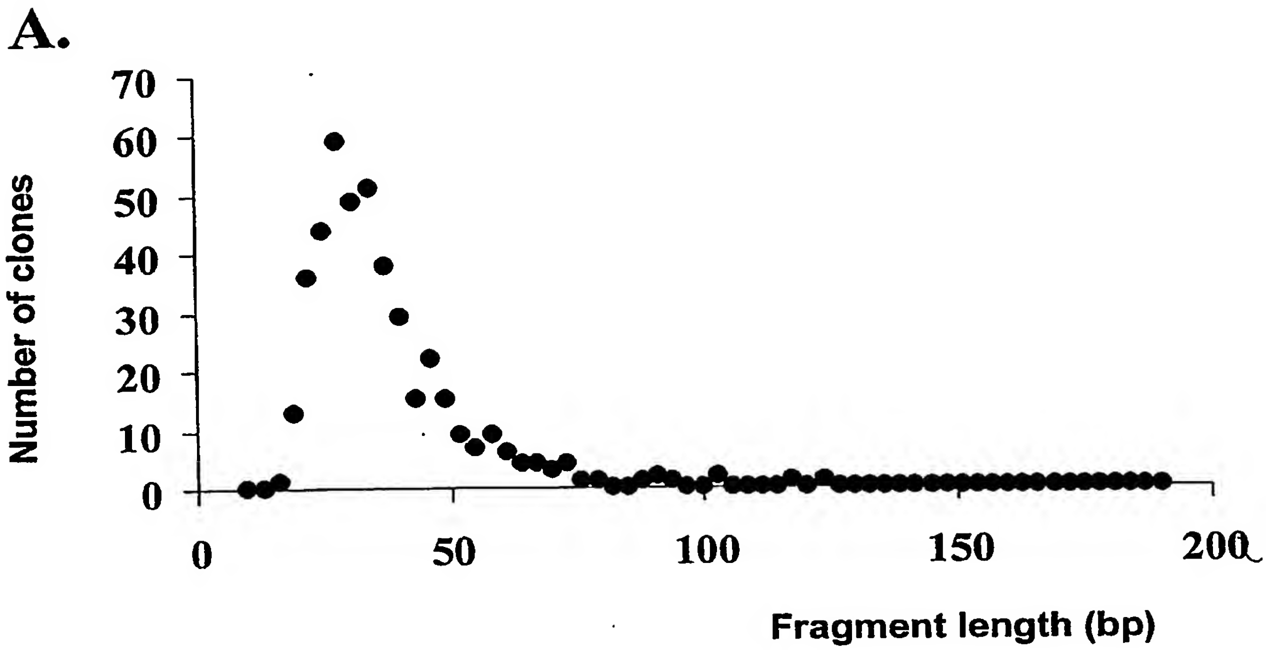
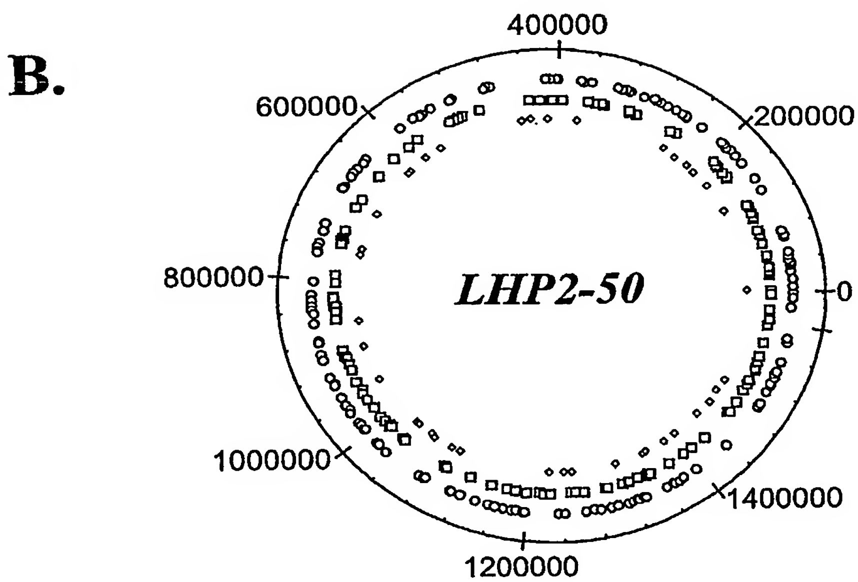


Total (trimmed)		562	(100,0 %)
ORF (+/+, +/-)	○	207	(36,8 %)
non-ORF (+/+, +/-)	□	185	(32,9 %)
chimeric	◇	88	(15,7 %)
non-blastable		82	(14,6 %)

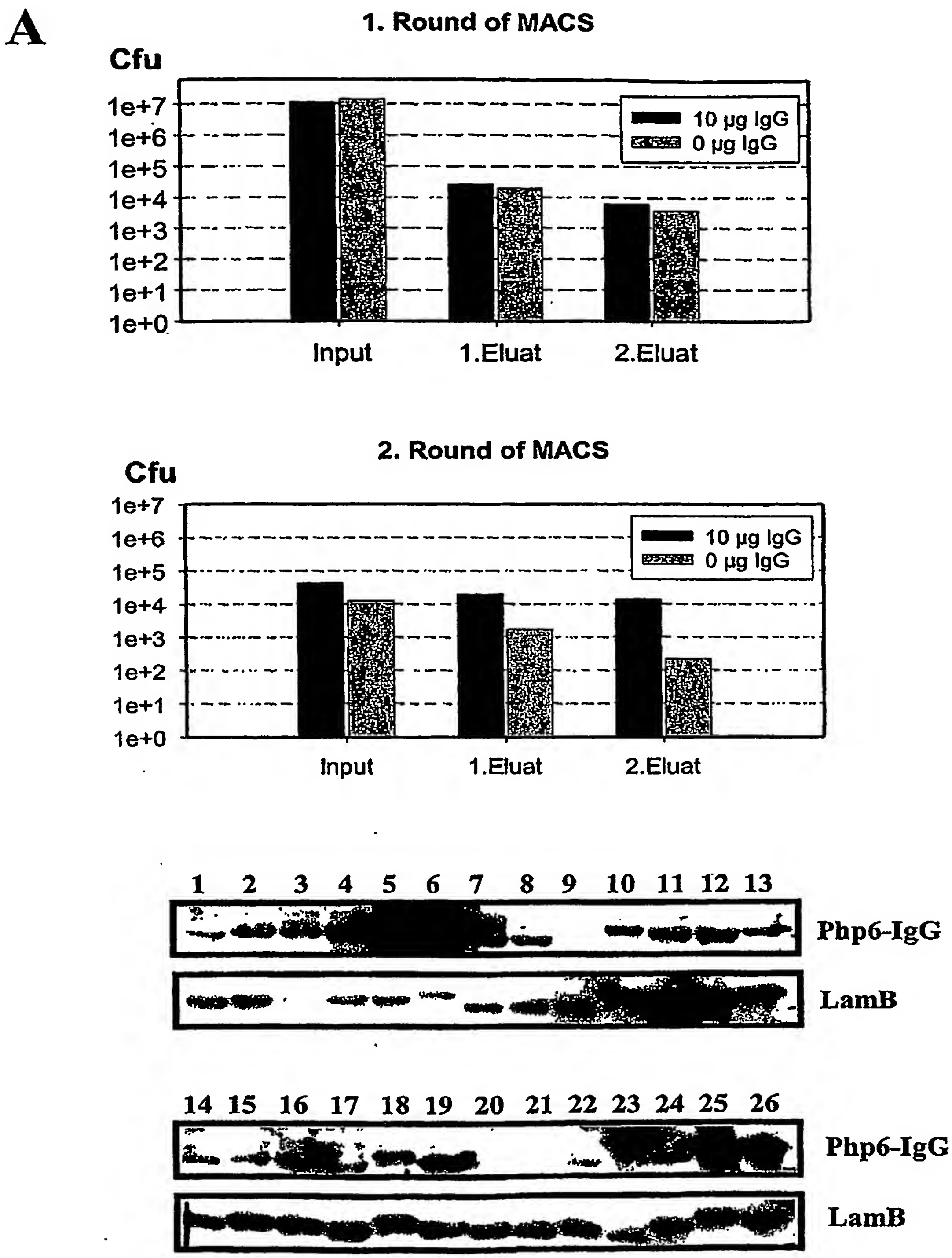
Figure 2





Total (trimmed)		439	(100,0 %)
ORF (+/+, +/-)	○	162	(36,9 %)
non-ORF (+/+, +/-)	□	141	(32,1 %)
chimeric	◇	40	(9,1 %)
non-blastable		96	(21,9 %)

Figure 3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2.Eluat
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Cfu
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1e+6
1e+5
1e+4
1e+3
1e+2
1e+1
1e+0
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0 µg IgG
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Figure 4

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<213> Helicobacter pylori

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<212> DNA
<213> Helicobacter pylori

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<212> DNA
<213> Helicobacter pylori

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<211> 1707

<212> DNA

<213> Helicobacter pylori

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<211> 1371

<212> DNA

<213> Helicobacter pylori

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<211> 2013
<212> DNA
<213> Helicobacter pylori

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<211> 693

<212> DNA

<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 897
<212> DNA
<213> Helicobacter pylori

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<210> 13

<211> 2436

<212> DNA

<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 858
<212> DNA
<213> Helicobacter pylori

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<211> 588

<212> DNA

<213> Helicobacter pylori

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<211> 1248

<212> DNA

<213> Helicobacter pylori

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<211> 2142

<212> DNA

<213> Helicobacter pylori

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<211> 1155

<212> DNA

<213> Helicobacter pylori

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<211> 1014

<212> DNA

<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 1863
<212> DNA
<213> Helicobacter pylori

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<211> 750

<212> DNA

<213> Helicobacter pylori

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<211> 1449

<212> DNA

<213> Helicobacter pylori

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<211> 1065

<212> DNA

<213> Helicobacter pylori

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<211> 1347

<212> DNA

<213> Helicobacter pylori

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<211> 1044

<212> DNA

<213> Helicobacter pylori

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<211> 1134
<212> DNA
<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 8679
<212> DNA
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<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 1287
<212> DNA
<213> Helicobacter pylori

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<211> 588
<212> DNA
<213> Helicobacter pylori

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cttttgcgcg atgaactcaa tcaagcgaga gaagaaattg aatttatgaa gaggaaatac 540
cgcttgatgt gggggaaagt cgctgacatg agcagcgtga ataaaaag 588

<210> 40
<211> 1524
<212> DNA
<213> Helicobacter pylori

<400> 40
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aaagccccca aaggtttgat tttgagtggg gggccagcga gcgtgtatgc taaagacgct 180

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<210> 41

<211> 804

<212> DNA

<213> Helicobacter pylori

<400> 41

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gagcaatatg aaaccaacaa agattcacca cctaaagaaa gaaaatacaa aaaatcaagc 180
gaattagaca atgcgatcaa acaatgcttg agagctaggg acttgccctt tagcgctgtg 240
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caaagaaaac aaagccgtag gtgt 804

<210> 42
<211> 2574
<212> DNA
<213> Helicobacter pylori

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<211> 1797
<212> DNA
<213> Helicobacter pylori

<400> 43
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<210> 44

<211> 942

<212> DNA

<213> Helicobacter pylori

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atgaaaatca accacactaa ggggttttgc gctaaaggcg tgttcctccc taatgcgcaa 180
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<210> 45
<211> 1356
<212> DNA
<213> Helicobacter pylori

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gaagagcgaa gaaaggcgct agaagcgggt aaaaaa 1356

<210> 46

<211> 828

<212> DNA

<213> Helicobacter pylori

<400> 46
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<210> 47

<211> 990

<212> DNA

<213> Helicobacter pylori

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<211> 5781

<212> DNA

<213> Helicobacter pylori

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<211> 1143

<212> DNA

<213> Helicobacter pylori

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aaa 1143

<210> 50
<211> 1110
<212> DNA
<213> Helicobacter pylori

<220>
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<223> "n" can be any base

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<210> 51

<211> 426

<212> DNA

<213> Helicobacter pylori

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gaaaccctag aacaaaaagt ggccgtactc aatgactata atgataagaa tgttaatatc 240

aagtttgaca acataagttt agggagtttt caacctaatg ataatctagg tatcaatgcg 300

atgtggggca ttcaaaatct tctcatgagc caaatgatgg gcgattacgg tccaaacaat 360

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gggtat 426

<210> 52

<211> 2949

<212> DNA

<213> Helicobacter pylori

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cccttttttta aagtcttgtt tgatgggggg aataggttgt ttggtttccc tgaaactttc 180

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<210> 53
<211> 621
<212> DNA
<213> Helicobacter pylori

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<210> 54
<211> 3558
<212> DNA
<213> Helicobacter pylori

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<211> 1248

<212> DNA

<213> Helicobacter pylori

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<211> 1020
<212> DNA
<213> Helicobacter pylori

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<211> 3084
<212> DNA
<213> Helicobacter pylori

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<211> 582

<212> DNA

<213> Helicobacter pylori

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<210> 59

<211> 1536

<212> DNA

<213> Helicobacter pylori

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<210> 60
<211> 2748
<212> DNA
<213> Helicobacter pylori

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<211> 1242

<212> DNA

<213> Helicobacter pylori

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<211> 1299

<212> DNA

<213> Helicobacter pylori

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<210> 63

<211> 1926

<212> DNA

<213> Helicobacter pylori

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<210> 64

<211> 2295

<212> DNA

<213> Helicobacter pylori

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<211> 2481

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<213> Helicobacter pylori

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<211> 819

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<213> Helicobacter pylori

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<211> 1242

<212> DNA

<213> Helicobacter pylori

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<211> 1734

<212> DNA

<213> Helicobacter pylori

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<211> 1044

<212> DNA

<213> Helicobacter pylori

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<211> 984

<212> DNA

<213> Helicobacter pylori

<400> 70

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<211> 1386
<212> DNA
<213> Helicobacter pylori

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<211> 357
<212> DNA
<213> Helicobacter pylori

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<211> 1581
<212> DNA
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<210> 75
<211> 1599
<212> DNA
<213> Helicobacter pylori

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<211> 1626

<212> DNA

<213> Helicobacter pylori

<400> 76

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<210> 77

<211> 873

<212> DNA

<213> Helicobacter pylori

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<211> 1515
<212> DNA
<213> Helicobacter pylori

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<210> 79

<211> 2373

<212> DNA

<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 7587

<212> DNA

<213> Helicobacter pylori

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<211> 579

<212> DNA

<213> Helicobacter pylori

<400> 85

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<213> Helicobacter pylori

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<211> 1461
<212> DNA
<213> Helicobacter pylori

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<213> Helicobacter pylori

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<211> 864

<212> DNA

<213> Helicobacter pylori

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<211> 885

<212> DNA

<213> Helicobacter pylori

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<211> 2574
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<213> Helicobacter pylori

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<211> 870

<212> DNA

<213> Helicobacter pylori

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<210> 94

<211> 2871

<212> DNA

<213> Helicobacter pylori

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<213> Helicobacter pylori

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<213> Helicobacter pylori

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<213> Helicobacter pylori

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<213> Helicobacter pylori

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<212> DNA

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<213> Helicobacter pylori

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<211> 909

<212> DNA

<213> Helicobacter pylori

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<211> 3633

<212> DNA

<213> Helicobacter pylori

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<211> 558

<212> DNA

<213> Helicobacter pylori

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cctttaaaaa tagaaagt 558

<210> 121

<211> 1437

<212> DNA

<213> Helicobacter pylori

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<211> 813

<212> DNA

<213> Helicobacter pylori

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<210> 123

<211> 1764

<212> DNA

<213> Helicobacter pylori

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aaactctatg agcttggcta tctt 1764

<210> 124

<211> 618

<212> DNA

<213> Helicobacter pylori

<400> 124

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gcgtctattt tgaaaaaaac aaaagggttt gaaaaaaatt tctcttggaa tgaggctgac 600

gctttgactt tagggtat 618

<210> 125

<211> 120

<212> DNA

<213> Helicobacter pylori

<400> 125

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gcgcatagac gagcgttatt tcaggcctac cgaagtggat ttgcttttag gcgatcccac 120

<210> 126

<211> 51

<212> DNA

<213> Helicobacter pylori

<400> 126
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<210> 127

<211> 204

<212> DNA

<213> Helicobacter pylori

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agagggcatg gggaggtttt ctttaaaaga aattttaatg ctcagcctta ccttattggc 120

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tgtcatggtt ttaatggcgt tttg 204

<210> 128

<211> 87

<212> DNA

<213> Helicobacter pylori

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gttgcttcta taataaattc cagagag 87

<210> 129

<211> 144

<212> DNA

<213> Helicobacter pylori

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gcattaagcc cactaaaaaa gaag 144

<210> 130

<211> 69

<212> DNA

<213> Helicobacter pylori

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tgtggcgtt 69

<210> 131

<211> 93

<212> DNA

<213> Helicobacter pylori

<400> 131
aaaaagctta taaaaagcct agcattaaag aaagacaccg ccatcgttat gaaatcaacc 60

ccaaataccg ccaagagtgg gaaaataagg gct 93

<210> 132

<211> 72

<212> DNA

<213> Helicobacter pylori

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cgcccaaact cc 72

<210> 133

<211> 54

<212> DNA

<213> Helicobacter pylori

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<210> 134

<211> 42

<212> DNA

<213> Helicobacter pylori

<400> 134
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<210> 135

<211> 60

<212> DNA

<213> Helicobacter pylori

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<210> 136

<211> 189

<212> DNA

<213> Helicobacter pylori

<400> 136
cgctttgaaa gacaaaacct atctctacgc tatggatcta ttggattaca acaactattt 60

atccatagaa aaccccatta tcaaaacaag agcaatggga acttatgcgg atttgattat 120

catcacaggc tcattagagc aagtcaatgg gtattacaac attctaaaag cgctcaacaa 180

acgcaacgc 189

<210> 137

<211> 147

<212> DNA

<213> Helicobacter pylori

<400> 137
tcgtcagttt catcaaaaaa gccagccaaa aattccctaa ctcgcttttt atcatcacag 60

gggatcattt tgacaggagc tatgaatacg ctaaaaacga tttgtatatc attaaatccg 120

tgccgcttat tttatatgcc cctactt 147

<210> 138

<211> 102

<212> DNA

<213> Helicobacter pylori

<400> 138
aagtggaaca tttctacccc aaaaccccca cccaagaatg gcgcgatagg gtgggggatt 60

atttcacttt tgagcaagac tatcttaata attttgggaa tc 102

<210> 139

<211> 81

<212> DNA

<213> Helicobacter pylori

<400> 139
aaaacgcgat ggataccaac agagaagtgg cgcaattcca ctatggaggc ggcacgccga 60

ccttttttc gcccattcaa t 81

<210> 140

<211> 228

<212> DNA

<213> Helicobacter pylori

<400> 140
aaaaactttc gtgctcatga cttttttgag cgcagggatt gtcaatattt ttattccgtc 60

tggcggaggg caatgggcga ttcaagctcc tatcatgctt ccggctgggc aaagcttagg 120

ggtggatccg ggagtggttt ctatggctat cgcttgggga gatgcttgga cgaatatgat 180

acagcctttt tgggctttgc ccgctttagc cattgcgggt ttgggcgc 228

<210> 141

<211> 72

<212> DNA

<213> Helicobacter pylori

<400> 141
aaggcccggt taaaacgctt tcagattatt ccacttatat cagccgaaaa agcaatgtta 60

caggcgatgc gt 72

<210> 142

<211> 51

<212> DNA

<213> Helicobacter pylori

<400> 142
cgggcaccat ttagacggga gccttggagg ttggggggt gctgtaattt a 51

<210> 143
<211> 69
<212> DNA
<213> Helicobacter pylori

<400> 143
tttacaaggc ataaacaaac aagccgctca aaaagaagca aaagccttag cgttaaaaat 60
ggggttaga 69

<210> 144
<211> 78
<212> DNA
<213> Helicobacter pylori

<400> 144
ttcttcagtt acattcaata tgaaaggcgc tctagtggct atcaccgagc ttggcccttc 60
tttagggagc gttttgac 78

<210> 145
<211> 63
<212> DNA
<213> Helicobacter pylori

<400> 145
agggatttac ttgcaatacc gcagcgtttt gcgcgaaaac aggcttttaa aaaaccatct 60
ctc 63

<210> 146
<211> 33
<212> DNA
<213> Helicobacter pylori

<400> 146
aaatcgccca aaaaggcaac aaaaaagagg ttt 33

<210> 147

<211> 39

<212> DNA

<213> Helicobacter pylori

<400> 147
gcgcttgagc agcgtgatga aagatttacc cgtgggggt 39

<210> 148

<211> 303

<212> DNA

<213> Helicobacter pylori

<400> 148
cccatatctt gcaaagcccc taaattcgtg gtgagtttgt gcaattctgg catgccgtta 60

gacttaggcc cttggaaagg caagaccgcc acaaagtccc tttctaattc tttattttta 120

aagcgttcta aaaactcgct ttgggtttta aaaacaatcg ctctagcctt aactttccta 180

tgctcatctt taatggctga gattttaatc acggccctcc ctaaattacc ctttaaaatt 240

ttaagccccc cattagcggc aaaaggatca ctaacagggc gtaaaatatc cgtattcagg 300

cta 303

<210> 149

<211> 45

<212> DNA

<213> Helicobacter pylori

<400> 149
aagagcatca catcacgcca agctataaaa ccgatattga gagcg 45

<210> 150

<211> 114

<212> DNA

<213> Helicobacter pylori

<400> 150
tttaaaaccc ttgttgagct ttttaaaagc caaataccag gtgcctttag aaaacattcg 60

catccaagac actcaaattt tagcgttttt aaaaaatccg gaaaaagtgg ggtt 114

<210> 151

<211> 93

<212> DNA

<213> Helicobacter pylori

<400> 151
aacgctatta tgaagccaaa gaaaccgcaa tatttaaaaa attccctaaa ttcatccaac 60

tttatgataa cgccacttct aaaatccaag cct 93

<210> 152

<211> 48

<212> DNA

<213> Helicobacter pylori

<400> 152
ataaaagccc taaaaccaag cttgtttgag cgtctaaatt ctctaaac 48

<210> 153

<211> 186

<212> DNA

<213> Helicobacter pylori

<400> 153
gcgatgctgt tttttagatt cgttacggtt tctcccacat acgcgcagcc ggctccccaa 60

gtgttagaag taaccgtgcc agatggcgtg ccacggagat tgccgtcgct accccttttca 120

tggcatactc ctaaagagtc tttcacgaac gctgcaggga ttctttcaaa gtccttcacc 180

actgct 186

<210> 154

<211> 105

<212> DNA

<213> Helicobacter pylori

<400> 154
gggctttttc aaaatctaac gccccactca aagacaccgc gctcacttcg ccgagcgaat 60

gccctaaagc aaaaacgggt tttaaccccc catttacttg cttgt 105

<210> 155

<211> 111

<212> DNA

<213> Helicobacter pylori

<400> 155
tttgttggac cccaagaggt gccaccgatc gcaacgccca agaaaaaccc aaaatgcaag 60

ttctcacgat tgaaaatagc cgggttaaac aacacatctg tgccagcccc a 111

<210> 156

<211> 291

<212> DNA

<213> Helicobacter pylori

<400> 156
ataagagcgt ttttcaaagg tgtaaatctt gccaatttca ttgactatgg gcgtgatagc 60

cgcatttttg ggagcgatga tttcataagc ggtgttagtg gtagtggtga atttgcatgc 120

aaaaaaacgc ccgtcttcgg ttatttcgcc attgacttga aaatcccctt cgctaatggc 180

tgtttggtgg ttttgagtat ccaacctttc aaaaggcctt cgcatcaaat agccgtccgt 240

aaaacccctg tttttaagcg tgttcaattc gctggcataa aaactcggct t 291

<210> 157

<211> 123

<212> DNA

<213> Helicobacter pylori

<400> 157
aagttcttta gcaatcactt gagaagaaag gtcgttttta tagatataag tttgcatgtc 60

aatgcttttt tggctcattc taataagtcc cactctatgc aacagagcgt caaagccatc 120

ttc 123

<210> 158

<211> 42

<212> DNA

<213> Helicobacter pylori

<400> 158
tccgtagggg tgaaaaaatc gcctccaaac tccacttccg ca 42

<210> 159

<211> 198

<212> DNA

<213> Helicobacter pylori

<400> 159
accctaactt gcaaaaaagt cgcttctaaa agggctttga tttgcgcatt gatttcgctc 60

acgctcaata catccaccag ctcccccttt tatagcaaac gagtgagatc attgaaaagc 120

cctaaaaaca tgataaaaac caaaaacccc acccccgcta gccacaacgc attttgtatg 180

ggtgttggca aagtgata 198

<210> 160

<211> 189

<212> DNA

<213> Helicobacter pylori

<400> 160
gcgtcaatga gtttgtctaa tcctgtgccg ctaggcatcg ccgcggttac gcctacgatt 60

ttttcatctt ttttagctaa ttctaaaagg gtgttagaat acgcttcagt gggcgataag 120

attgcgcttt tggatttttt agacaagccg gtatccaaat caaaaggccc caccccatgc 180

catttttca 189

<210> 161

<211> 255

<212> DNA

<213> Helicobacter pylori

<400> 161
atctttttga gcaacacctc tctttgcatg gggcggacaa attgcaacac aaaaagcaat 60

gaaaacgcgc tcgcttcttt aaactcaacc tctaaaaaat ccatgcattc aaaacgggca 120

ttgttaaaat cttttaattt ttcttgcgct tttttgagca tgggcatgga attatcaatc 180

cctacaagct caatctcttg ttggatttgt cggttaagcg cgataaaaaa gttcccggta 240

gaacagccca aatca 255

<210> 162

<211> 249

<212> DNA

<213> Helicobacter pylori

<400> 162
agggattttc aagtccttaa acatcgcttg caccctttct ttttcatttt tacgcaacaa 60

gccatgatcc acaaaaacag cgatcaaatt atccttaatg gctctgtgca acagcgtagc 120

gaccaccgta gaatccacgc ccccactcac cgcgcacaaa accttagcgt tagcgatttt 180

ttctttcaat cgtgcgattt ctctttgagc gaaatgctgc atcccccaag ttttttcaca 240

gccgcaaac 249

<210> 163

<211> 117

<212> DNA

<213> Helicobacter pylori

<400> 163
attatccaca tgaggggcga ccactctcat cacatgccct cttttttca gcgcttcaaa 60

aaaacgaaac gctgtcatag aagtgccatt actggtgtct ttaaaactat ccacgac 117

<210> 164

<211> 132

<212> DNA

<213> Helicobacter pylori

<400> 164
atcattatcc cggctgtgct cgccaatgac catgcccaca taaaccttcg tttgggggtt 60

gataaaaagc gtgcctcttt cttggatatt gaaaagggaa aaagcggtcg cttcgccatt 120

ttccatgctg at 132

<210> 165

<211> 75

<212> DNA

<213> Helicobacter pylori

<400> 165
aaaaaccgcc cttctaaaaa cccgctcgcg caaaacgccg tagtgagcgc gttagctccg 60

ggcaaaacat cgtat 75

<210> 166

<211> 66

<212> DNA

<213> Helicobacter pylori

<400> 166
aaaccctcta gcgtttggat ctataaacca ataataaggg gcaaaaatat tcaaaccata 60

ccttcc 66

<210> 167

<211> 147

<212> DNA

<213> Helicobacter pylori

<400> 167
tcgtcagttt catcaaaaaa gccagccaaa aattccctaa ctcgcttttt atcatcacag 60

gggatcattt tgacaggagc tatgaatacg ctaaaaacga tttgtatatc attaaatccg 120

tgccgcttat tttatatgcc cctactt 147

<210> 168

<211> 129

<212> DNA

<213> Helicobacter pylori

<400> 168
cgcgctcgct cgcgctctct tttaggattt tttcttttga aagcgagttg caaaacaccg 60

cataagagcc taaattttca tctttccaat tcaaaacagg gtaagtggcg cataaaatct 120

ttttggaaa 129

<210> 169

<211> 261

<212> DNA

<213> Helicobacter pylori

<400> 169
gtttcagaaa tcttatccac gctcgttagc ccatcaaaac tccctgagga accaaaggct 60

aaattgatgc gttgggggc atcagcgcca tttttagggt caaattgcaa aagaggcggg 120

ttcatgcctg caagcgatcc gtcgttatta aaatgcaaac ggcctccttc aaacacatta 180

ggcctagccg ctgaccccсс tactaattcc ccaggctcag gcacgatcac cctaaaattc 240

cattccgctc ccccactcct a 261

<210> 170

<211> 108

<212> DNA

<213> Helicobacter pylori

<400> 170
ctgcctaacc ttaacaaaat cagttcatca tctttcacta aatacacaag caaaacatca 60

ggcttaatgt ggcattccct aaaaggtttc cactttccct ttaaggca 108

<210> 171

<211> 78

<212> DNA

<213> Helicobacter pylori

<400> 171
tcaaggttta gggagcgtgt tgccgccctc tttacaaaac gcgctcaaag aaaacgattt 60

aggcactctt ttatcgcc 78

<210> 172

<211> 123

<212> DNA

<213> Helicobacter pylori

<400> 172
aatattcatt ggccacacgc accaaatcgc tcacttttaa atccaaaaat tgtcgctggt 60

aatccgtcaa gccttgaata tcgttttgca ctaaatagtc cgcaaaaagc cccgcaacat 120

cgc 123

<210> 173

<211> 303

<212> DNA

<213> Helicobacter pylori

<400> 173
cccatatctt gcaaagcccc taaattcgtg gtgagtttgt gcaattctgg catgccgtta 60

gacttaggcc cttggaaagg caagaccgcc acaaagtccc tttctaattc tttattttta 120

aagcgttcta aaaactcgct ttgggtttta aaaacaatcg ctctagcctt aactttccta 180

tgctcatctt taatggctga gattttaatc acggccctcc ctaaattacc ctttaaaatt 240

ttaagccccc cattagcggc aaaaggatca ctaacagggc gtaaaatatc cgtattcagg 300

cta 303

<210> 174

<211> 81

<212> DNA

<213> Helicobacter pylori

<400> 174

gaatctttag tcctaaaacc tattttaggc aaacggcgtt gtaagggttg ttgccctcct 60

tcaaagcctc ttttagcctt a 81

<210> 175

<211> 84

<212> DNA

<213> Helicobacter pylori

<400> 175

ggttcaaatg agcgatcgca taaggagcga ttaagtattc aaacccatag aattgcttca 60

agagattttg atatttgtcc tctt 84

<210> 176

<211> 276

<212> DNA

<213> Helicobacter pylori

<400> 176

ctaggggca ataaatcttt cacgctatac tcccaccaca catcacagcc ttttttctca 60

aaaagattgg ccacatgctc taaaacttcg ctttcaaaac aaggcttatt cgtgcgtttg 120

tctatgaaaa aggccagtgg cacgccccat tttctttgcc ggctcaagca ccaatcaggg 180

cggttttcta tcatggtttt taggcggttt ttcccgctgc ttggcacaaa ttccaccttt 240

tcaatcgcat ctaaagccac ttctcttaag gttttt 276

<210> 177

<211> 99

<212> DNA

<213> Helicobacter pylori

<400> 177
gcgttcgtgc ttaagccttg taaaaaagcc tgctcttgga gttttaagtt ttccttggct 60

aattccacgc tagaaagcaa gcttttgtat tctttcaaa 99

<210> 178

<211> 186

<212> DNA

<213> Helicobacter pylori

<400> 178
gagagcatct cttctctgat cctgtcaaaa ataatgatcg tatcattaat ggaataccca 60

atcaaggtga gcaaggccgc aatcacttcc aaattcatat caatcttaaa aacaatcacc 120

gagcttgcca ctaaaatcac atcatgcaca agcgcaatga cgctcgctaa agcaaaacgc 180

cattca 186

<210> 179

<211> 634

<212> PRT

<213> Helicobacter pylori

<400> 179

Met Val Lys Asn Thr Gly Glu Leu Lys Lys Leu Ser Asp Thr Tyr Glu
1   5   10   15

Asn Leu Ser Asn Leu Leu Thr Asn Phe Asn Asn Leu Asn Gln Ala Val
            20   25   30

Thr Asn Ala Ser Ser Pro Ser Glu Ile Asn Ala Thr Ile Asp Asn Leu
        35   40   45

Lys Ala Asn Thr Gln Gly Leu Ile Gly Glu Lys Thr Asn Ser Pro Ala
    50   55   60

Tyr Gln Ala Val Tyr Leu Ala Leu Asn Ala Ala Val Gly Leu Trp Asn
65   70   75   80

Val Ile Ala Tyr Asn Val Gln Cys Gly Pro Gly Lys Ser Gly Asp Gln
                85   90   95

Ser Val Ile Phe Asp Gly Gln Pro Gly His Asp Ser Arg Ser Ile Asn
100 105 110

Cys Asn Leu Thr Gly Tyr Asn Asn Gly Val Ser Gly Pro Leu Ser Ile
115 120 125

Asp Asn Phe Lys Thr Leu Asn Gln Ala Tyr Gln Thr Ile Gln Gln Ala
130 135 140

Leu Lys Gln Asp Ser Gly Phe Pro Val Leu Asp Ser Lys Gly Lys Gln
145 150 155 160

Val Thr Ile Lys Ile Thr Thr Gln Thr Asn Gly Ala Asn Lys Ser Glu
165 170 175

Thr Thr Thr Thr Thr Thr Thr Thr Asn Asp Ala Gln Thr Leu Leu Gln
180 185 190

Glu Ala Ser Lys Met Ile Ser Val Leu Thr Thr Asn Cys Pro Trp Val
195 200 205

Asn Thr Ala His Asn Ser Asn Gly Gly Ala Pro Trp Asn Leu Asn Thr
210 215 220

Thr Gly Asn Val Cys Gln Val Phe Ala Thr Glu Phe Ser Ala Val Thr
225 230 235 240

Ser Met Ile Lys Asn Ala Gln Glu Ile Val Thr Gln Ala Gln Ser Leu
245 250 255

Asn Asn Pro Gln Ser Asn Gln Asn Ala Pro Lys Asp Phe Asn Pro Tyr
260 265 270

Thr Ser Ala Asp Arg Ala Phe Ala Gln Asn Met Leu Asn His Ala Gln
275 280 285

Ala Gln Ala Lys Met Leu Glu Leu Ala Asp Gln Met Lys Lys Asp Leu
290 295 300

Asn Thr Ile Pro Lys Gln Phe Ile Thr Asn Tyr Leu Ala Ala Cys Arg
305 310 315 320

Asn Gly Gly Gly Thr Leu Pro Asp Ala Gly Val Thr Ser Asn Thr Trp
325 330 335

Gly Ala Gly Cys Ala Tyr Val Glu Glu Thr Ile Thr Ala Leu Asn Asn
340 345 350

Ser Leu Ala His Phe Gly Thr Gln Ala Asp Gln Ile Lys Gln Ser Glu
355 360 365

Leu Leu Ala Arg Thr Ile Leu Asp Phe Arg Gly Ser Leu Lys Asp Leu
370 375 380

Asn Asn Thr Tyr Asn Ser Ile Thr Thr Thr Ala Ser Asn Thr Pro Asn
385 390 395 400

Ser Pro Phe Leu Lys Asn Leu Ile Ser Gln Ser Thr Asn Pro Asn Asn
405 410 415

Pro Gly Gly Leu Gln Ala Val Tyr Gln Val Asn Gln Ser Ala Tyr Ser
420 425 430

Gln Leu Leu Ser Ala Thr Gln Glu Leu Gly His Asn Pro Phe Arg Arg
435 440 445

Val Gly Leu Ile Ser Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile
450 455 460

Gly Val Gln Ile Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Arg Trp
465 470 475 480

Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Tyr Ile Lys
485 490 495

Ser Ser Phe Phe Asn Ser Ala Ser Asp Val Phe Thr Tyr Gly Val Gly
500 505 510

Thr Asp Val Leu Tyr Asn Phe Ile Asn Asp Lys Ala Thr Lys Asn Asn
515 520 525

Lys Ile Ser Phe Gly Val Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser
530 535 540

Trp Leu Asn Ser Gln Tyr Val Asn Leu Ala Thr Phe Asn Asn Phe Tyr
545 550 555 560

Ser Ala Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Leu Gly
565 570 575

Leu Arg Met Asn Leu Ala Lys Asn Lys Lys Lys Ala Ser Asp His Val
580 585 590

Ala Gln His Gly Val Glu Leu Gly Val Lys Ile Pro Thr Ile Asn Thr
595 600 605

Asn Tyr Tyr Ser Leu Leu Gly Thr Gln Leu Gln Tyr Arg Arg Leu Tyr
610 615 620

Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
625 630

<210> 180

<211> 546

<212> PRT

<213> Helicobacter pylori

<400> 180

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
1   5   10   15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
            20   25   30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
        35   40   45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro
    50   55   60

Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr
65   70   75   80

Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr
                85   90   95

Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro
            100   105   110

Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn
        115   120   125

Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr
    130   135   140

Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu
145   150   155   160

Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val
                165   170   175

Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met
            180   185   190

Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu
        195   200   205

Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys
    210   215   220

Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met
225 230 235 240

Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu
245 250 255

Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile
260 265 270

Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu
275 280 285

Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu
290 295 300

Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly
305 310 315 320

Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly
325 330 335

His Ser His Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile
340 345 350

Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu
355 360 365

Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser
370 375 380

Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser
385 390 395 400

Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala
405 410 415

Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp
420 425 430

Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu
435 440 445

Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn
450 455 460

Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly
465 470 475 480

Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val
485 490 495

Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu
500 505 510

Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Ala Pro
515 520 525

Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly
530 535 540

Met Met
545

<210> 181

<211> 470

<212> PRT

<213> Helicobacter pylori

<400> 181

Met Lys Ile Lys Asn Ile Leu Leu Ser Gly Gly Ser Gly Lys Arg Leu
1 5 10 15

Trp Pro Leu Ser Arg Ser Leu Tyr Pro Lys Gln Phe Leu Lys Leu Phe
20 25 30

Asp His Lys Ser Leu Phe Glu Leu Ser Phe Lys Arg Asn Ala Ser Leu
35 40 45

Val Asp Glu Thr Leu Ile Val Cys Asn Glu Lys His Tyr Phe Leu Ala
50 55 60

Leu Glu Glu Ile Lys Asn Glu Ile Lys Asn Lys Ser Val Gly Phe Leu
65 70 75 80

Leu Glu Ser Leu Ser Lys Asn Thr Ala Asn Ala Ile Ala Leu Ser Ala
85 90 95

Leu Met Ser Asp Lys Glu Asp Leu Leu Ile Val Thr Pro Ser Asp His
100 105 110

Leu Ile Lys Asp Leu Gln Ala Tyr Glu Asn Ala Ile Lys Lys Ala Ile
115 120 125

Asp Leu Ala Gln Lys Gly Phe Leu Val Thr Phe Gly Val Ser Ile Asp
130 135 140

Lys Pro Asn Thr Glu Phe Gly Tyr Ile Glu Ser Pro Asn Gly Leu Asp
145 150 155 160

Val Lys Arg Phe Ile Glu Lys Pro Ser Leu Asp Lys Ala Ile Glu Phe
165 170 175

Gln Lys Ser Gly Gly Phe Tyr Phe Asn Ser Gly Met Phe Val Phe Gln
180 185 190

Ala Gly Val Phe Leu Asp Glu Leu Lys Lys His Ala Pro Thr Ile Leu
195 200 205

Lys Gly Cys Glu Arg Ala Phe Glu Ser Leu Glu Asn Ala Tyr Phe Phe
210 215 220

Glu Lys Lys Ile Ala Arg Leu Ser Glu Lys Ser Met Gln Asp Leu Glu
225 230 235 240

Asp Met Ser Ile Asp Ile Ala Leu Met Gln Gln Ser His Lys Ile Lys
245 250 255

Met Val Glu Leu Asn Ala Lys Trp Ser Asp Leu Gly Asn Phe Asn Ala
260 265 270

Leu Phe Glu Glu Ala Ala Asn Glu Pro Lys Glu Asn Val Ser Leu Asn
275 280 285

Gln Thr Pro Val Phe Ala Lys Glu Ser Glu Asn Asn Leu Val Phe Ser
290 295 300

His Lys Val Ser Ala Leu Leu Gly Val Glu Asn Leu Ala Val Ile Asp
305 310 315 320

Thr Lys Asp Ala Leu Leu Ile Ala His Lys Asp Lys Ala Lys Asp Leu
325 330 335

Lys Ala Leu Val Asn Glu Val Glu Thr Asn Asn Gln Glu Leu Leu Gln
340 345 350

Thr His Thr Lys Val Tyr Arg Pro Trp Gly Ser Tyr Glu Val Leu His
355 360 365

Glu Ser Gly Cys Tyr Lys Val Lys Ile Leu Glu Val Lys Pro Asn Ala
370 375 380

Arg Leu Ser Leu Gln Lys His Phe His Arg Ser Glu His Trp Val Val
385 390 395 400

Ile Ser Gly Met Ala Ser Val Glu Leu Asp His Gln Leu Phe Glu Leu
405 410 415

Gln Ala Asn Glu Ser Thr Tyr Ile Pro Lys Asn Thr Leu His Arg Leu
420 425 430

Ala Asn Tyr Gly Lys Ile Pro Leu Ile Ile Ile Glu Val Gln Val Gly
435 440 445

Glu Tyr Val Gly Glu Asp Asp Ile Val Arg Ile Asp Asp Asp Phe Asn
450 455 460

Arg Gln Asn Gln Asn Ala
465 470

<210> 182

<211> 496

<212> PRT

<213> Helicobacter pylori

<400> 182

Met Ala Glu Trp Lys Thr Asp Thr Glu Glu Val Lys Glu Val Val Lys
1 5 10 15

Lys Cys Arg Glu Phe Lys Arg Ser Leu Gln Glu Glu Lys Cys Ser Pro
20 25 30

Phe Ile Lys Asp Leu Asp Ser Tyr Ala Leu Lys Ile Ile Val Glu Arg
35 40 45

Arg Lys Ile Glu His Gln Leu Gln Glu Ala Ile Glu Lys Leu Arg Arg
50 55 60

Ala Lys Lys Lys Arg Ser Ser Phe Trp Gly Ser Phe Val Glu Gly Ala
65 70 75 80

Arg Asp Leu Leu Asp Met Val Arg Glu Ile Ile Pro Pro Ala Lys Leu
85 90 95

Gly Ala Glu Ala Cys Asp Lys Val Leu Asn Leu Met Glu Asp Asn Ile
100 105 110

Glu Lys Trp Glu His Asn Val Arg Leu Leu Glu Arg Met Leu Glu Ile
115 120 125

Tyr Ala Thr Gln Ala Lys Ala Ser Ala Glu Leu Val Glu Gly Ala Trp
130 135 140

Lys Ser Val Lys Lys Ser Leu Asp Phe Tyr Thr Asp Lys His Gln Glu
145 150 155 160

Phe Ile Lys Arg Leu Asn Tyr Ala Ser Glu Ala Ile Asp Asn Glu Tyr
165 170 175

Asn Ile Ala Pro Pro Glu Ile Leu Asn Glu Ser Asp Phe Glu Ser Pro
180 185 190

Thr Ile Val Tyr Asn Pro Lys Lys Ser Val Tyr Asp Glu His Leu Lys
195 200 205

Asp Leu Arg Glu Asp Phe Ser Phe Ser Leu Tyr Ala Asp Leu Lys Asn
210 215 220

Arg Ile Asn Ala Ser Ser Lys Leu Asp Arg Thr Thr Thr Ser Lys Glu
225 230 235 240

Gln Glu Phe Glu Lys Asn Leu Glu Asp Leu Met Pro Gly Phe Arg Gly
245 250 255

Gly Thr Asp Thr Leu Ser Gly Asp Glu Leu Glu His Met Ala Ser Phe
260 265 270

Arg Gly Gln Glu Phe Glu Lys Asn Leu Glu Asp Leu Met Pro Ser Ser
275 280 285

Leu Gly Val His Ser Tyr Asp Glu Ser Leu Asn Leu Ala Lys Lys Asn
290 295 300

Cys Val Lys Asn Cys Lys Lys Ala Leu Gly Asp Phe Thr Glu Lys Ile
305 310 315 320

Lys Glu Ser Pro Asn Asp Leu Asn Ala Ile Asn Glu Ala Phe Asn His
325 330 335

Leu Glu Thr Glu Leu Glu Arg Ala Thr Glu Asn Leu Ser Gln Lys Ile
340 345 350

Ala Pro Ile Leu Glu Arg Tyr Glu Asn Asp Lys Arg Gln Lys Leu Gly
355 360 365

Tyr Gly Glu Phe Leu Glu Lys Glu Lys Glu Gly Phe Met Val Asp Glu
370 375 380

Gln Asn Pro Tyr Pro Glu Glu Val Arg Phe Asn Glu Leu Arg Leu Ala
385 390 395 400

Glu Phe Glu Ser Val Phe Ser Ala Ile Val Pro Leu Glu Asp Leu Asp
405 410 415

Lys Pro Ala Cys Ala His His Ala Leu Lys Ala Leu Glu Ala Thr Leu
420 425 430

Lys Asn Arg Asp Leu Gly Phe Asp Ala Thr Glu Leu Glu Gln Ile Ala
435 440 445

Lys Gly Phe Ile Pro Lys Gly Tyr Leu Trp His Phe Asp Ala Asn Val
450 455 460

Leu Gly Asn Val Ala Leu Val Arg Glu Glu Leu Leu Leu Gly Val Lys
465 470 475 480

His Thr Lys Gly Tyr Leu Leu Trp Lys Gln Phe Leu Gln Thr Gln Asn
485 490 495

<210> 183

<211> 265

<212> PRT

<213> Helicobacter pylori

<400> 183

Met Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile
1 5 10 15

Gly Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro
20 25 30

Phe Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile
35 40 45

Met Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp
50 55 60

Val Gln Leu Asn Ile Gly Pro Asn Cys Lys Leu Arg Ile Thr Ser Gln
65 70 75 80

Ser Phe Glu Lys Ile His Asn Thr Glu Asp Gly Phe Ala Ser Arg Asp
85 90 95

Met His Ile Val Val Gly Glu Asn Ala Phe Leu Asp Phe Ala Pro Phe
100 105 110

Pro Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile
115 120 125

Ser Leu Arg Ser Ser Ser Gln Leu Leu Tyr Ser Glu Ile Ile Val Ala
130 135 140

Gly Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr
145 150 155 160

Lys Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr
165 170 175

Ile Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp
180 185 190

Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu
195 200 205

Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu Gly Val Asp Gly
210 215 220

Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala
225 230 235 240

Lys Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu
245 250 255

Val Thr Gln Thr Thr Thr Gln Lys Val
260 265

<210> 184

<211> 569

<212> PRT

<213> Helicobacter pylori

<400> 184

Met Lys Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr
1 5 10 15

Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Ile Ala Glu Val
20 25 30

Glu His Asp Tyr Thr Ile Tyr Gly Glu Glu Leu Lys Phe Gly Gly Gly
35 40 45

Lys Thr Leu Arg Glu Gly Met Ser Gln Ser Asn Asn Pro Ser Lys Glu
50 55 60

Glu Leu Asp Leu Ile Ile Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly
65 70 75 80

Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile
85 90 95

Gly Lys Gly Gly Asn Lys Asp Met Gln Asp Gly Val Lys Asn Asn Leu
100 105 110

Ser Val Gly Pro Ala Thr Glu Ala Leu Ala Gly Glu Gly Leu Ile Val
115 120 125

Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln
130 135 140

Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly
145 150 155 160

Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg
165 170 175

Arg Asn Leu Lys Trp Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn
180 185 190

Leu Gly Phe Leu Ala Lys Gly Asn Ala Ser Asn Asp Ala Ser Leu Ala
195 200 205

Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp
210 215 220

Gly Thr Thr Pro Ser Ala Ile Asn His Ala Leu Asp Val Ala Asp Lys
225 230 235 240

Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly
245 250 255

Cys Val Glu Asp Thr Met Ala Ala Ile Ala Gly Arg Thr Met His Thr
260 265 270

Phe His Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Ile Ile Lys
275 280 285

Val Ala Gly Glu His Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile
290 295 300

Pro Phe Thr Val Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val
305 310 315 320

Cys His His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp
325 330 335

Ser Arg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Thr Leu His Asp
340 345 350

Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg
355 360 365

Val Gly Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys
370 375 380

Lys Glu Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe
385 390 395 400

Arg Ile Lys Arg Tyr Leu Ser Lys Tyr Thr Ile Asn Pro Ala Ile Ala
405 410 415

His Gly Ile Ser Glu Tyr Val Gly Ser Val Glu Val Gly Lys Val Ala
420 425 430

Asp Leu Val Leu Trp Ser Pro Ala Phe Phe Gly Val Lys Pro Asn Met
435 440 445

Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
450 455 460

Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala
465 470 475 480

His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln
485 490 495

Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln
500 505 510

Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln
515 520 525

Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His
530 535 540

Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val
545 550 555 560

Ser Leu Ala Gln Leu Phe Ser Ile Phe
565

<210> 185

<211> 450

<212> PRT

<213> Helicobacter pylori

<400> 185

Met Ser Met Glu Phe Asp Ala Val Ile Ile Gly Gly Gly Val Ser Gly
1 5 10 15

Cys Ala Thr Phe Tyr Thr Leu Ser Glu Tyr Ser Ser Leu Lys Arg Val
20 25 30

Ala Ile Val Glu Lys Cys Ser Lys Leu Ala Gln Ile Ser Ser Ser Ala
35 40 45

Lys Ala Asn Ser Gln Thr Ile His Asp Gly Ser Ile Glu Thr Asn Tyr
50 55 60

Thr Pro Glu Lys Ala Lys Lys Val Arg Leu Ser Ala Tyr Lys Thr Arg
65 70 75 80

Gln Tyr Ala Leu Asn Lys Gly Leu Gln Asn Glu Val Ile Phe Glu Thr
85 90 95

Gln Lys Met Ala Ile Gly Val Gly Asp Glu Glu Cys Glu Phe Met Lys
100 105 110

Lys Arg Tyr Glu Ser Phe Lys Glu Ile Phe Val Gly Leu Glu Glu Phe
115 120 125

Asp Lys Gln Lys Ile Lys Glu Leu Glu Pro Asn Val Ile Leu Gly Ala
130 135 140

Asn Gly Ile Asp Arg His Glu Asn Ile Ile Gly His Gly Tyr Arg Lys
145 150 155 160

Asp Trp Ser Thr Met Asn Phe Ala Lys Leu Ser Glu Asn Phe Val Glu
165 170 175

Glu Ala Leu Lys Leu Lys Pro Asn Asn Gln Val Phe Leu Asn Phe Lys
180 185 190

Val Lys Lys Ile Glu Lys Arg Asn Asp Thr Tyr Ala Val Ile Ser Glu
195 200 205

Asp Ala Glu Glu Val Tyr Ala Lys Phe Val Leu Val Asn Ala Gly Ser
210 215 220

Tyr Ala Leu Pro Leu Ala Gln Ser Met Gly Tyr Gly Leu Asp Leu Gly
225 230 235 240

Cys Leu Pro Val Ala Gly Ser Phe Tyr Phe Val Pro Asp Leu Leu Arg
245 250 255

Gly Lys Val Tyr Thr Val Gln Asn Pro Lys Leu Pro Phe Ala Ala Val
260 265 270

His Gly Asp Pro Asp Ala Val Ile Lys Gly Lys Thr Arg Ile Gly Pro
275 280 285

Thr Ala Leu Thr Met Pro Lys Leu Glu Arg Asn Lys Cys Trp Leu Lys
290 295 300

Gly Ile Ser Leu Glu Leu Leu Lys Met Asp Leu Asn Lys Asp Val Phe
305 310 315 320

Lys Ile Ala Phe Asp Leu Met Ser Asp Lys Glu Ile Arg Asn Tyr Val
325 330 335

Phe Lys Asn Met Val Phe Glu Leu Pro Ile Ile Gly Lys Arg Lys Phe
340 345 350

Leu Lys Asp Ala Gln Lys Ile Ile Pro Ser Leu Ser Leu Glu Asp Leu
355 360 365

Glu Tyr Ala His Gly Phe Gly Glu Val Arg Pro Gln Val Leu Asp Arg
370 375 380

Thr Lys Arg Lys Leu Glu Leu Gly Glu Lys Lys Ile Cys Thr His Lys
385 390 395 400

Gly Ile Thr Phe Asn Met Thr Pro Ser Pro Gly Ala Thr Ser Cys Leu
405 410 415

Gln Asn Ala Leu Val Asp Ser Gln Glu Ile Ala Ala Tyr Leu Gly Glu
420 425 430

Ser Phe Glu Leu Glu Arg Phe Tyr Lys Asp Leu Ser Pro Glu Glu Leu
435 440 445

Glu Asn
450

<210> 186

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 186

Met Arg Tyr Phe Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr
1 5 10 15

Lys Lys Asp Phe Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser
20 25 30

Ser Tyr Leu Ala Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile
35 40 45

Asp Pro Gln Ala Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala
50 55 60

Trp Tyr Ser Pro Trp Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu
65 70 75 80

Val Phe Trp Ile Leu Lys Glu Met Asn Lys Ser Thr Gly Tyr Gly Glu
85 90 95

Asp Leu Lys Pro Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser
100 105 110

Met Asp Ile Glu His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala
115 120 125

Arg Asp Ser Asp Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu
130 135 140

Ser Gln Lys Gly Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe
145 150 155 160

Gln Gly Thr Pro Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr
165 170 175

Ala His Ile Gln Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp
180 185 190

Leu Val Tyr Met His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys
195 200 205

Asp Tyr Val Met Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr
210 215 220

Gly Asp Phe Tyr Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile
225 230 235 240

Pro Gln Ser Gln Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys
245 250 255

Ala Tyr Gly Phe Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser
260 265 270

Val Ile Leu Glu Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn
275 280 285

Ser Glu Asn Met Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr
290 295 300

Gly Trp Gly Gly Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg
305 310 315 320

Asp Ser Phe Ala Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala
325 330 335

Gln Ser Arg Tyr Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala
340 345 350

Lys Glu Lys Glu Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr
355 360 365

Leu Ile Tyr Leu Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn
370 375 380

His Gln Ala Ile Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys
385 390 395 400

His Phe Lys Thr Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser
405 410 415

Leu Trp Leu Ala Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu
420 425 430

Leu Ile Asp Arg Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn
435 440 445

Lys Thr Ser Ser Pro Leu Asn Ala Asn
450 455

<210> 187

<211> 671

<212> PRT

<213> Helicobacter pylori

<400> 187

Met Lys Lys Lys Ala Asn Glu Glu Lys Ala Gln Lys Arg Ala Lys Thr
1 5 10 15

Glu Ala Lys Ala Glu Ala Thr Gln Glu Asn Lys Thr Lys Glu Asn Asn
20 25 30

Lys Ala Lys Glu Ser Lys Ile Lys Glu Ser Lys Ile Lys Glu Ala Lys
35 40 45

Ala Lys Glu Pro Ile Pro Val Lys Lys Leu Ser Phe Asn Glu Ala Leu
50 55 60

Glu Glu Leu Phe Ala Asn Ser Leu Ser Asp Cys Val Ser Tyr Glu Ser
65 70 75 80

Ile Ile Gln Ile Ser Ala Lys Val Pro Thr Leu Ala Gln Ile Lys Lys
85 90 95

Ile Lys Glu Leu Cys Gln Lys Tyr Gln Lys Lys Leu Val Ser Ser Ser
100 105 110

Glu Tyr Ala Lys Lys Leu Asn Ala Ile Asp Lys Ile Lys Lys Thr Glu
115 120 125

Glu Lys Gln Lys Val Leu Asp Glu Glu Leu Glu Asp Gly Tyr Asp Phe
130 135 140

Leu Lys Glu Lys Asp Phe Leu Glu Trp Ser Arg Ser Asp Ser Pro Val
145 150 155 160

Arg Met Tyr Leu Arg Glu Met Gly Asp Ile Lys Leu Leu Ser Lys Asp
165 170 175

Glu Glu Ile Glu Leu Ser Lys Gln Ile Arg Leu Gly Glu Asp Ile Ile
180 185 190

Leu Asp Ala Ile Cys Ser Val Pro Tyr Leu Ile Asp Phe Ile Tyr Ala
195 200 205

Tyr Lys Asp Ala Leu Ile Asn Arg Glu Arg Arg Val Lys Glu Leu Phe
210 215 220

Arg Ser Phe Asp Asp Asp Asp Glu Asn Ser Val Ser Asp Ser Lys Lys
225 230 235 240

Asp Glu Asp Asn Glu Glu Asp Glu Glu Asn Glu Glu Arg Lys Lys Val
245 250 255

Val Ser Glu Lys Asp Lys Lys Arg Val Glu Lys Val Gln Glu Ser Phe
260 265 270

Lys Ala Leu Asp Lys Ala Lys Lys Glu Trp Leu Lys Ala Leu Glu Ala
275 280 285

Pro Ile Asp Glu Arg Glu Asp Glu Leu Val Arg Ser Leu Thr Leu Ala
290 295 300

Tyr Lys Arg Gln Thr Leu Lys Asp Arg Leu Tyr Asp Leu Glu Pro Thr
305 310 315 320

Ser Lys Leu Ile Asn Glu Leu Val Lys Thr Met Glu Thr Thr Leu Lys
325 330 335

Ser Gly Asp Gly Phe Glu Lys Glu Leu Lys Arg Leu Glu Tyr Lys Leu
340 345 350

Pro Leu Phe Asn Asp Thr Leu Ile Ala Asn His Lys Lys Ile Leu Ala
355 360 365

Asn Ile Thr Asn Met Thr Lys Glu Asp Ile Ile Ala Gln Val Pro Glu
370 375 380

Ala Thr Met Val Ser Val Tyr Met Asp Leu Lys Lys Leu Phe Leu Thr
385 390 395 400

Lys Glu Ala Ser Glu Glu Gly Phe Asp Leu Ala Pro Asn Lys Leu Lys
405 410 415

Glu Ile Leu Glu Gln Ile Lys Arg Gly Lys Leu Ile Ser Asp Arg Ala
420 425 430

Lys Asn Lys Met Ala Lys Ser Asn Leu Arg Leu Val Val Ser Ile Ala
435 440 445

Lys Arg Phe Thr Ser Arg Gly Leu Pro Phe Leu Asp Leu Ile Gln Glu
450 455 460

Gly Asn Ile Gly Leu Met Lys Ala Val Asp Lys Phe Glu His Glu Lys
465 470 475 480

Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Lys Gln Ala Ile
485 490 495

Ser Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile Pro Ile His
500 505 510

Met Ile Asp Thr Ile Asn Arg Ile Asn Lys Val Met Arg Lys His Ile
515 520 525

Gln Glu Asn Gly Lys Glu Pro Asp Leu Glu Val Val Ala Glu Glu Val
530 535 540

Gly Leu Ser Leu Asp Lys Val Lys Asn Val Ile Lys Val Thr Lys Glu
545 550 555 560

Pro Ile Ser Leu Glu Thr Pro Val Gly Asn Asp Asp Asp Gly Lys Phe
565 570 575

Gly Asp Phe Val Glu Asp Lys Asn Ile Val Ser Ser Ile Asp His Ile
580 585 590

Met Arg Glu Asp Leu Lys Ala Gln Ile Glu Ser Val Leu Asp Gln Leu
595 600 605

Asn Glu Arg Glu Lys Ala Val Ile Arg Met Arg Phe Gly Leu Leu Asp
610 615 620

Asp Glu Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys Glu Leu Asn Val
625 630 635 640

Thr Arg Glu Arg Val Arg Gln Ile Glu Ser Ser Ala Ile Lys Lys Leu
645 650 655

Arg Ser Pro Gln Tyr Gly Arg Ile Leu Arg Asn Tyr Leu Arg Ile
660 665 670

<210> 188

<211> 231

<212> PRT

<213> Helicobacter pylori

<400> 188

Met Val Gln Lys Ile Gly Ile Leu Gly Ala Met Arg Glu Glu Ile Thr
1 5 10 15

Pro Ile Leu Glu Leu Phe Gly Val Asp Phe Glu Glu Ile Pro Leu Gly
20 25 30

Gly Asn Val Phe His Lys Gly Val Tyr His Asn Lys Glu Ile Ile Val
35 40 45

Ala Tyr Ser Lys Ile Gly Lys Val His Ser Thr Leu Thr Thr Thr Ser
50 55 60

Met Ile Leu Ala Phe Gly Val Gln Lys Val Leu Phe Ser Gly Val Ala
65 70 75 80

Gly Ser Leu Val Lys Asp Leu Lys Ile Asn Asp Leu Leu Val Ala Ile
85 90 95

Gln Leu Val Gln His Asp Val Asp Leu Ser Ala Phe Asp His Pro Leu
100 105 110

Gly Phe Ile Pro Glu Ser Ala Ile Phe Ile Glu Thr Ser Glu Ser Leu
115 120 125

Asn Ala Leu Ala Lys Glu Val Ala Asn Glu Gln His Ile Val Leu Lys
130 135 140

Glu Gly Val Ile Ala Ser Gly Asp Gln Phe Val His Ser Lys Glu Arg
145 150 155 160

Lys Glu Phe Leu Val Ser Glu Phe Lys Ala Ser Ala Val Glu Met Glu
165 170 175

Gly Ala Ser Val Ala Phe Val Cys Gln Lys Phe Gly Val Pro Cys Cys
180 185 190

Val Leu Arg Ser Ile Ser Asp Asn Ala Asp Glu Glu Ala Asn Met Ser
195 200 205

Phe Asp Ala Phe Leu Glu Lys Ser Ala Gln Thr Ser Ala Lys Phe Leu
    210   215   220

Lys Ser Met Val Asp Glu Leu
225   230

<210> 189

<211> 514

<212> PRT

<213> Helicobacter pylori

<400> 189

Met Ser Phe Arg Ile Asn Thr Asn Ile Ala Ala Leu Thr Ser His Ala
1   5   10   15

Val Gly Val Gln Asn Asn Arg Asp Leu Ser Ser Ser Leu Glu Lys Leu
            20   25   30

Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ser Ser Gly Met
        35   40   45

Ala Ile Ala Asp Ser Leu Arg Ser Gln Ser Ala Asn Leu Gly Gln Ala
    50   55   60

Ile Arg Asn Ala Asn Asp Ala Ile Gly Met Val Gln Thr Ala Asp Lys
65   70   75   80

Ala Met Asp Glu Gln Ile Lys Ile Leu Asp Thr Ile Lys Thr Lys Ala
                85   90   95

Val Gln Ala Ala Gln Asp Gly Gln Thr Leu Glu Ser Arg Arg Ala Leu
            100   105   110

Gln Ser Asp Ile Gln Arg Leu Leu Glu Glu Leu Asp Asn Ile Ala Asn
        115   120   125

Thr Thr Ser Phe Asn Gly Gln Gln Met Leu Ser Gly Ser Phe Ser Asn
    130   135   140

Lys Glu Phe Gln Ile Gly Ala Tyr Ser Asn Ala Thr Val Lys Ala Ser
145   150   155   160

Ile Gly Ser Thr Ser Ser Asp Lys Ile Gly His Val Arg Met Glu Thr
                165   170   175

Ser Ser Phe Ser Gly Ala Gly Met Leu Ala Ser Ala Ala Ala Gln Asn
            180   185   190

Leu Thr Glu Val Gly Leu Asn Phe Lys Gln Val Asn Gly Val Asn Asp
195 200 205

Tyr Lys Ile Glu Thr Val Arg Ile Ser Thr Ser Ala Gly Thr Gly Ile
210 215 220

Gly Ala Leu Ser Glu Ile Ile Asn Arg Phe Ser Asn Thr Leu Gly Val
225 230 235 240

Arg Ala Ser Tyr Asn Val Met Ala Thr Gly Gly Thr Pro Val Gln Ser
245 250 255

Gly Thr Val Arg Glu Leu Thr Ile Asn Gly Val Glu Ile Gly Thr Val
260 265 270

Asn Asp Val His Lys Asn Asp Ala Asp Gly Arg Leu Thr Asn Ala Ile
275 280 285

Asn Ser Val Lys Asp Arg Thr Gly Val Glu Ala Ser Leu Asp Ile Gln
290 295 300

Gly Arg Ile Asn Leu His Ser Ile Asp Gly Arg Ala Ile Ser Val His
305 310 315 320

Ala Ala Ser Ala Ser Gly Gln Val Phe Gly Gly Gly Asn Phe Ala Gly
325 330 335

Ile Ser Gly Thr Gln His Ala Val Ile Gly Arg Leu Thr Leu Thr Arg
340 345 350

Thr Asp Ala Arg Asp Ile Ile Val Ser Gly Val Asn Phe Ser His Val
355 360 365

Gly Phe His Ser Ala Gln Gly Val Ala Glu Tyr Thr Val Asn Leu Arg
370 375 380

Ala Val Arg Gly Ile Phe Asp Ala Asn Val Ala Ser Ala Ala Gly Ala
385 390 395 400

Asn Ala Asn Gly Ala Gln Ala Glu Thr Asn Ser Gln Gly Ile Gly Ala
405 410 415

Gly Val Thr Ser Leu Lys Gly Ala Met Ile Val Met Asp Met Ala Asp
420 425 430

Ser Ala Arg Thr Gln Leu Asp Lys Ile Arg Ser Asp Met Gly Ser Val
435 440 445

Gln Met Glu Leu Val Thr Thr Ile Asn Asn Ile Ser Val Thr Gln Val
450 455 460

Asn Val Lys Ala Ala Glu Ser Gln Ile Arg Asp Val Asp Phe Ala Glu
465 470 475 480

Glu Ser Ala Asn Phe Ser Lys Tyr Asn Ile Leu Ala Gln Ser Gly Ser
485 490 495

Phe Ala Met Ala Gln Ala Asn Ala Val Gln Gln Asn Val Leu Arg Leu
500 505 510

Leu Gln

<210> 190

<211> 299

<212> PRT

<213> Helicobacter pylori

<400> 190

Met Lys Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr
1 5 10 15

Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His
20 25 30

Asn Thr Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val
35 40 45

Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg
50 55 60

Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala
65 70 75 80

Leu Ile Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys
85 90 95

Thr Glu Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala
100 105 110

Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu
115 120 125

Glu Val Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr
130 135 140

Asn Ala Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg
145 150 155 160

His Ile Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu
165 170 175

Ile Asp Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu
180 185 190

Ala Asn Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly
195 200 205

Gly Asp Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser
210 215 220

Lys Ala Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val
225 230 235 240

Lys Thr Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser
245 250 255

Pro Val Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met
260 265 270

Leu Gln Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu
275 280 285

Leu Arg Lys His Ala Lys Ile Val Ile Asn Lys
290 295

<210> 191

<211> 812

<212> PRT

<213> Helicobacter pylori

<400> 191

Val Arg Tyr Ile Lys Phe Phe Lys Glu Leu Asn Asn Lys Asn Val Asn
1 5 10 15

Leu Val Gly Gly Lys Asn Ala Ser Ile Gly Glu Met Phe Gln Glu Leu
20 25 30

Val Pro Ile Gly Ile Lys Val Pro Asp Gly Phe Ala Ile Thr Ser Glu
35 40 45

Ala Tyr Trp Tyr Leu Leu Glu Gln Gly Gly Ala Lys Gln Lys Ile Ile
50 55 60

Glu Leu Leu Glu Asn Val Asp Ala Thr Glu Ile Asp Val Leu Lys Ile
65 70 75 80

Arg Ser Lys Gln Ile Arg Glu Leu Ile Phe Gly Thr Pro Phe Pro Ser
85 90 95

Asp Leu Arg Asp Glu Ile Phe Gln Ala Tyr Glu Ile Leu Ser Gln Gln
100 105 110

Tyr His Met Lys Glu Ala Asp Val Ala Val Arg Ser Ser Ala Thr Ala
115 120 125

Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu
130 135 140

Asn Ile Lys Gly Lys Thr Glu Leu Ile His Tyr Ile Lys Ser Cys Leu
145 150 155 160

Ala Ser Leu Phe Thr Asp Arg Ala Ile Ser Tyr Arg Ala Ser Arg Gly
165 170 175

Phe Asp His Leu Lys Val Ala Leu Ser Val Gly Val Gln Lys Met Val
180 185 190

Arg Ala Asp Lys Gly Ser Ala Gly Val Met Phe Ser Ile Asp Thr Glu
195 200 205

Thr Gly Phe Lys Asp Ala Val Phe Ile Thr Ser Ala Trp Gly Leu Gly
210 215 220

Glu Asn Val Val Gly Gly Thr Ile Asn Pro Asp Glu Phe Tyr Val Phe
225 230 235 240

Lys Pro Thr Leu Glu Gln Asn Lys Arg Pro Ile Ile Lys Arg Gln Leu
245 250 255

Gly Asn Lys Thr Gln Lys Met Val Tyr Ala Pro Arg Gly Ser Glu His
260 265 270

Pro Thr Arg Asn Ile Lys Thr Thr Lys Lys Glu Trp Gln Ser Phe Ser
275 280 285

Leu Ser Asp Glu Asp Val Leu Ile Leu Ala Lys Tyr Ala Ile Glu Ile
290 295 300

Glu Lys His Tyr Ser Lys Glu Ala Lys Gln Tyr Arg Pro Met Asp Ile
305 310 315 320

Glu Trp Ala Lys Asp Gly Glu Ser Gly Glu Ile Phe Ile Val Gln Ala
325 330 335

Arg Pro Glu Thr Val Gln Ser Gln Lys Ser Lys Glu Glu Ser Gln Val
340 345 350

Phe Glu Lys Phe Lys Phe Lys Asn Pro Asn Glu Lys Lys Glu Ile Ile
355 360 365

Leu Gln Gly Arg Ala Ile Gly Ser Lys Ile Gly Ser Gly Lys Val Arg
370 375 380

Ile Ile Asn Asp Leu Glu His Met Asn Ser Phe Lys Glu Gly Glu Ile
385 390 395 400

Leu Val Thr Asp Asn Thr Asp Pro Asp Trp Glu Pro Cys Met Lys Lys
405 410 415

Ala Ser Ala Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala
420 425 430

Ile Val Ala Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly
435 440 445

Ala Thr Asp Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala
450 455 460

Glu Gly Glu Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile
465 470 475 480

Glu Arg Val Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr
485 490 495

Ile Asn Ile Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro
500 505 510

Asn His Gly Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln
515 520 525

Ile Lys Ala His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser
530 535 540

Val Lys Glu Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn
545 550 555 560

Pro Lys Asp Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile
565 570 575

Ser Ala Ala Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe
580 585 590

Lys Ser Asn Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro
595 600 605

Asn Glu Glu Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr
610 615 620

Ser Glu Ser Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala
625 630 635 640

Leu Val Arg Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro
645 650 655

Phe Leu Arg Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg
660 665 670

Lys Asn Asn Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met
675 680 685

Cys Glu Leu Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu
690 695 700

Phe Asp Gly Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu
705 710 715 720

Gly Val Asp Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg
725 730 735

Asn Glu Ala Met Leu Lys Met Phe Lys Lys Ala Ile Glu Ala Cys Lys
740 745 750

Arg His Asn Lys Tyr Cys Gly Ile Cys Gly Gln Ala Pro Ser Asp Tyr
755 760 765

Pro Glu Val Thr Glu Phe Leu Val Lys Glu Gly Ile Thr Ser Ile Ser
770 775 780

Leu Asn Pro Asp Ser Val Ile Pro Thr Trp Asn Ala Val Ala Lys Leu
785 790 795 800

Glu Lys Glu Leu Lys Glu His Gly Leu Thr Glu His
805 810

<210> 192

<211> 612

<212> PRT

<213> Helicobacter pylori

<400> 192

Met Ser Ala Glu Leu Ile Ala Val Tyr Lys Asp Glu Gln Ile Ile Asp
1 5 10 15

Leu Glu Ser Ala Lys Val Leu Gly Leu Ser Asp Gly Ile Lys Ala Leu
20 25 30

Asn Gly Thr Glu Pro Ile Tyr Phe Asp Asp Ser Pro Leu Ala Leu Glu
35 40 45

Val Ile Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala
50 55 60

Leu Tyr Pro Asp Ala Lys Phe Phe Val Gly Pro Val Val Glu Glu Gly
65 70 75 80

Phe Tyr Tyr Asp Phe Lys Thr Ser Ser Lys Ile Ser Glu Glu Asp Leu
85 90 95

Pro Lys Ile Glu Ala Lys Met Lys Glu Phe Ala Lys Leu Lys Leu Ala
100 105 110

Ile Thr Lys Glu Thr Leu Thr Arg Glu Gln Ala Leu Glu Arg Phe Lys
115 120 125

Gly Asp Glu Leu Lys His Ala Val Met Ser Lys Ile Gly Gly Asp Ala
130 135 140

Phe Gly Val Tyr Gln Gln Gly Glu Phe Glu Asp Leu Cys Lys Gly Pro
145 150 155 160

His Leu Pro Asn Thr Arg Phe Leu Asn His Phe Lys Leu Thr Lys Leu
165 170 175

Ala Gly Ala Tyr Leu Gly Gly Asp Glu Asn Asn Glu Met Leu Ile Arg
180 185 190

Ile Tyr Gly Ile Ala Phe Ala Thr Lys Glu Gly Leu Lys Asp Tyr Leu
195 200 205

Phe Gln Ile Glu Glu Ala Lys Lys Arg Asp His Arg Lys Leu Gly Val
210 215 220

Glu Leu Gly Leu Phe Ser Phe Asp Asp Glu Ile Gly Ala Gly Leu Pro
225 230 235 240

Leu Trp Leu Pro Lys Gly Ala Arg Leu Arg Lys Arg Ile Glu Asp Leu
245 250 255

Leu Ser Gln Ala Leu Leu Leu Arg Gly Tyr Glu Pro Val Lys Gly Pro
260 265 270

Glu Ile Leu Lys Ser Asp Val Trp Lys Ile Ser Gly His Tyr Asp Asn
275 280 285

Tyr Lys Glu Asn Met Tyr Phe Thr Thr Ile Asp Glu Gln Glu Tyr Gly
290 295 300

Ile Lys Pro Met Asn Cys Val Gly His Ile Lys Val Tyr Gln Ser Ala
305   310   315   320

Leu His Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val
                325   330   335

Val His Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val
            340   345   350

Arg Glu Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln
        355   360   365

Ile Gln Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met
    370   375   380

Gln Ala Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala
385   390   395   400

Lys Ser Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu
                405   410   415

Lys Glu Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly
            420   425   430

Gly Gly Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala
        435   440   445

Leu Lys Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu
    450   455   460

Pro Glu Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu
465   470   475   480

Gln Pro Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe
                485   490   495

Ile Ala Ile Leu Ser Glu His Phe Gly Gly Asn Phe Pro Phe Phe Val
            500   505   510

Ala Pro Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val
        515   520   525

Phe Ala Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val
    530   535   540

Glu Val Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala
545   550   555   560

Glu Lys Gln Lys Ile Pro Met Ile Leu Val Leu Gly Asn Glu Glu Val
                565   570   575

Glu Thr Glu Ile Leu Ser Ile Arg Asp Arg Glu Lys Gln Asp Gln Tyr
580 585 590

Lys Met Pro Leu Lys Glu Phe Leu Asn Met Val Glu Ser Lys Met Gln
595 600 605

Glu Val Ser Phe
610

<210> 193

<211> 286

<212> PRT

<213> Helicobacter pylori

<400> 193

Val Lys Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg
1 5 10 15

Ala Glu Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val
20 25 30

Met Phe Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg
35 40 45

Val Leu Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe
50 55 60

Asn Arg Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe
65 70 75 80

Gly Ala Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile
85 90 95

Cys Tyr Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp
100 105 110

Arg Glu Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu
115 120 125

Ser Leu Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala
130 135 140

Leu His Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu
145 150 155 160

Ile Ser Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp
165 170 175

Ala Ile Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys
180 185 190

Ala Ala Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp
195 200 205

Ser Pro Glu Phe Ile Ser Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn
210 215 220

Ser Asp Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala
225 230 235 240

Ser Lys Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys
245 250 255

Lys Arg Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln
260 265 270

Glu Phe Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys
275 280 285

<210> 194

<211> 196

<212> PRT

<213> Helicobacter pylori

<400> 194

Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met Ser Val Leu Ile
1 5 10 15

Leu Gly Leu Gly Ile Val Val Phe Leu Val Val Phe Ala Leu Lys Asn
20 25 30

Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His Asn Glu Val Asp
35 40 45

Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn Phe Lys Ser Asn
50 55 60

Tyr Arg Phe Leu Val Gly Leu Lys Pro Leu Ile Lys Ser Pro Lys Thr
65 70 75 80

Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly Asp Lys Lys Leu
85 90 95

Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu Lys Ser Asn Thr
100 105 110

Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu Asp Ser Pro Asn
        115   120   125

Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Pro Ser Gln Pro Arg Trp
    130   135   140

Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro Leu Lys Phe Asp
145   150   155   160

Leu Leu Glu Ser Asp Lys Met Gly Arg Tyr Lys Ile Leu Phe Lys Phe
                165   170   175

Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln Leu Ala Phe Phe
            180   185   190

Lys Gln Arg Ile
        195

<210> 195

<211> 416

<212> PRT

<213> Helicobacter pylori

<400> 195

Met Ala Tyr Phe Leu Glu Gln Thr Asp Ser Glu Ile Phe Glu Leu Ile
1   5   10   15

Phe Glu Glu Tyr Lys Arg Gln Asn Glu His Leu Glu Met Ile Ala Ser
            20   25   30

Glu Asn Tyr Thr Phe Ala Ser Val Met Glu Ala Met Gly Ser Val Leu
        35   40   45

Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Asn Lys Arg Tyr Tyr Gly Gly
    50   55   60

Cys Glu Val Val Asp Lys Ile Glu Ser Leu Ala Ile Glu Arg Ala Lys
65   70   75   80

Lys Leu Phe Asn Cys Gln Phe Ala Asn Val Gln Ala His Ser Gly Ser
                85   90   95

Gln Ala Asn Asn Ala Val Tyr His Ala Leu Leu Lys Pro Tyr Asp Lys
            100   105   110

Ile Leu Gly Met Asp Leu Ser Cys Gly Gly His Leu Thr His Gly Ala
        115   120   125

Lys Val Ser Leu Thr Gly Lys His Tyr Gln Ser Phe Ser Tyr Gly Val
130 135 140

Asn Leu Asp Gly Tyr Ile Asp Tyr Glu Glu Ala Leu Lys Ile Ala Gln
145 150 155 160

Ser Val Lys Pro Glu Ile Ile Val Cys Gly Phe Ser Ala Tyr Pro Arg
165 170 175

Glu Ile Asp Phe Lys Lys Phe Arg Glu Ile Ala Asp Glu Val Gly Ala
180 185 190

Leu Leu Leu Gly Asp Ile Ala His Val Ala Gly Leu Val Val Thr Gly
195 200 205

Glu His Ala His Pro Phe Pro His Cys His Val Val Ser Ser Thr Thr
210 215 220

His Lys Thr Leu Arg Gly Pro Arg Gly Gly Ile Ile Leu Thr Asn Asp
225 230 235 240

Glu Glu Ile Ala Ala Lys Ile Asp Lys Ala Ile Phe Pro Gly Thr Gln
245 250 255

Gly Gly Pro Leu Met His Val Ile Ala Ala Lys Ala Val Gly Phe Lys
260 265 270

Glu Asn Leu Lys Pro Glu Phe Lys Ala Tyr Ala Gln Leu Val Lys Ser
275 280 285

Asn Met Gln Val Leu Ala Lys Ala Leu Lys Glu Lys Asn His Lys Leu
290 295 300

Val Ser Gly Gly Thr Ser Asn His Leu Leu Leu Met Asp Phe Leu Asp
305 310 315 320

Lys Pro Tyr Ser Gly Lys Asp Ala Asp Ile Ala Leu Gly Asn Ala Gly
325 330 335

Ile Thr Val Asn Lys Asn Thr Ile Pro Gly Glu Thr Arg Ser Pro Phe
340 345 350

Val Thr Ser Gly Ile Arg Ile Gly Ser Ala Ala Leu Ser Ala Arg Gly
355 360 365

Met Gly Ala Lys Glu Phe Glu Ile Ile Gly Asn Lys Ile Ser Asp Ile
370 375 380

Leu Asn Asp Ile Asn Asn Val Ser Leu Gln Leu His Val Lys Glu Glu
385 390 395 400

Leu Lys Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe
405 410 415

<210> 196

<211> 714

<212> PRT

<213> Helicobacter pylori

<400> 196

Met Lys Ile Thr Tyr Cys Asp Ala Leu Ile Ile Gly Gly Gly Leu Ala
1 5 10 15

Gly Leu Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile
20 25 30

Val Leu Ser Leu Val Pro Val Arg Arg Ser His Ser Ala Ala Ala Gln
35 40 45

Gly Gly Met Gln Ala Ser Leu Ala Asn Ala Lys Lys Ser Glu Gly Asp
50 55 60

Asn Glu Asp Leu His Phe Leu Asp Thr Val Lys Gly Ser Asp Trp Gly
65 70 75 80

Cys Asp Gln Gln Val Ala Arg Met Phe Val Thr Thr Ala Pro Lys Ala
85 90 95

Ile Arg Glu Leu Ala Ser Trp Gly Val Pro Trp Thr Arg Ile Lys Lys
100 105 110

Gly Asp Arg Pro Ala Val Val Asn Gly Glu His Val Thr Ile Thr Glu
115 120 125

Arg Asp Asp Arg His Gly Tyr Ile Leu Ser Arg Asp Phe Gly Gly Thr
130 135 140

Lys Lys Trp Arg Thr Cys Phe Thr Ala Asp Ala Thr Gly His Thr Met
145 150 155 160

Leu Tyr Ala Val Ala Asn Glu Ala Leu His His Lys Val Asp Ile Gln
165 170 175

Asp Arg Lys Asp Met Leu Ala Phe Ile His His Asp Asn Lys Cys Tyr
180 185 190

Gly Ala Val Val Arg Asp Leu Ile Thr Gly Glu Ile Ser Ala Tyr Val
195 200 205

Ser Lys Gly Thr Leu Leu Ala Thr Gly Gly Tyr Gly Arg Val Tyr Lys
210 215 220

His Thr Thr Asn Ala Val Ile Cys Asp Gly Ala Gly Ala Ala Ser Ala
225 230 235 240

Leu Glu Thr Gly Val Ala Lys Leu Gly Asn Met Glu Ala Val Gln Phe
245 250 255

His Pro Thr Ala Leu Val Pro Ser Gly Ile Leu Met Thr Glu Gly Cys
260 265 270

Arg Gly Asp Gly Gly Val Leu Arg Asp Lys Phe Gly Arg Arg Phe Met
275 280 285

Pro Ala Tyr Glu Pro Glu Lys Lys Glu Leu Ala Ser Arg Asp Val Val
290 295 300

Ser Arg Arg Ile Leu Glu His Ile Gln Lys Gly Tyr Gly Ala Lys Ser
305 310 315 320

Pro Tyr Gly Asp His Val Trp Leu Asp Ile Ala Ile Leu Gly Arg Asn
325 330 335

His Val Glu Lys Asn Leu Arg Asp Val Arg Asp Ile Ala Met Thr Phe
340 345 350

Ala Gly Ile Asp Pro Ala Asp Ser Lys Glu Gln Thr Lys Asp Asn Met
355 360 365

Gln Gly Val Pro Ala Asn Glu Pro Glu Tyr Gly Gln Ala Met Ala Lys
370 375 380

Gln Lys Gly Trp Ile Pro Ile Lys Pro Met Gln His Tyr Ser Met Gly
385 390 395 400

Gly Val Arg Thr Asn Pro Lys Gly Glu Thr His Leu Lys Gly Leu Phe
405 410 415

Cys Ala Gly Glu Ala Ala Cys Trp Asp Leu His Gly Phe Asn Arg Leu
420 425 430

Gly Gly Asn Ser Val Ser Glu Ala Val Val Ala Gly Met Ile Ile Gly
435 440 445

Asp Tyr Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr
450 455 460

Gln Lys Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe
465 470 475 480

Leu Leu His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg
485 490 495

Met Lys Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys
500 505 510

Arg Leu Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser
515 520 525

Lys Asn Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu
530 535 540

Glu Asp Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile
545 550 555 560

Thr Gln Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg
565 570 575

Ile Asp Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu
580 585 590

Ala Ser Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu
595 600 605

Glu Leu Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr
610 615 620

Gly Lys Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp
625 630 635 640

Ala Glu Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp
645 650 655

Arg Ile Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys
660 665 670

Tyr Lys Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg
675 680 685

Gly Glu His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His
690 695 700

Asn Ala Asn Leu Lys Gly Glu His His Glu
705 710

<210> 197

<211> 385

<212> PRT

<213> Helicobacter pylori

<400> 197

Met Lys Asp Ser Phe Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His
1   5   10   15

Pro Asp Lys Met Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Tyr Ile
            20   25   30

Ile Glu Arg Asp Gln Lys Ala Lys Val Ala Cys Glu Thr Leu Val Ser
        35   40   45

Asn Gly Phe Cys Met Ile Thr Gly Glu Leu Lys Thr Ser Val Tyr Ala
    50   55   60

Pro Met Gln Glu Ile Ala Arg Glu Val Val Lys Lys Ile Gly Tyr Thr
65   70   75   80

Asp Ala Leu Tyr Gly Phe Asp Tyr Arg Ser Ala Ala Val Leu Asn Gly
                85   90   95

Val Gly Glu Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Glu Asp
            100   105   110

Gly Glu Ile Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Cys
        115   120   125

Lys Glu Thr Glu Thr Leu Met Pro Leu Pro Ile His Leu Ala His Gln
    130   135   140

Leu Thr Phe Ala Leu Ala Gln Lys Arg Lys Asp Asn Thr Leu Pro Phe
145   150   155   160

Leu Arg Pro Asp Gly Lys Ser Gln Val Ser Val Arg Tyr Glu Asn Asn
                165   170   175

Lys Pro Val Ser Ile Asp Thr Ile Val Ile Ser Thr Gln His Ser Pro
            180   185   190

Glu Val Ser Gln Lys His Leu Lys Glu Ala Val Ile Glu Glu Ile Val
        195   200   205

Tyr Lys Val Leu Ser Lys Glu Tyr Leu His Asp Asn Ile Lys Phe Phe
    210   215   220

Val Asn Pro Thr Gly Lys Phe Val Ile Gly Gly Pro Gln Gly Asp Ala
225   230   235   240

Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Ser Cys
                245   250   255

Pro His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp
260 265 270

Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Leu Val Ala
275 280 285

Ser Gly Val Cys Asp Lys Ala Thr Val Gln Leu Ala Tyr Ala Ile Gly
290 295 300

Val Ile Glu Pro Val Ser Ile Tyr Val Asn Thr His Asn Thr Ser Lys
305 310 315 320

Tyr Ser Ser Ala Glu Leu Glu Lys Cys Val Lys Ser Val Phe Lys Leu
325 330 335

Thr Pro Lys Gly Ile Ile Glu Ser Leu Asp Leu Leu Arg Pro Ile Tyr
340 345 350

Ser Leu Thr Ser Ala Tyr Gly His Phe Gly Arg Glu Leu Glu Glu Phe
355 360 365

Thr Trp Glu Lys Thr Asn Lys Ala Glu Glu Ile Lys Ala Phe Phe Lys
370 375 380

Arg
385

<210> 198

<211> 338

<212> PRT

<213> Helicobacter pylori

<400> 198

Met Met Lys Ile Val Ile Asp Leu Met Gly Ala Asp His Gly Val Leu
1 5 10 15

Pro Val Ile Glu Gly Val Ser Arg Ala Leu Glu Asn Lys Ser Phe Ser
20 25 30

Thr Val Leu Val Gly Asp Lys Asp Lys Ala Thr Pro Phe Ile Ser Lys
35 40 45

Glu Leu Ala Ser Lys Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys
50 55 60

Met Glu Glu Ala Ala Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile
65 70 75 80

Tyr Leu Gly Met Asp Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser
85 90 95

Ala Gly His Ser Gly Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly
100 105 110

Arg Ile Lys Gly Val Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser
115 120 125

Val Gly Lys Arg Pro Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp
130 135 140

Cys Lys Pro Glu Tyr Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr
145 150 155 160

Ala Lys Ser Val Leu His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser
165 170 175

Asn Gly Glu Glu Asp Ile Lys Gly Asn Met Leu Val Lys Glu Thr His
180 185 190

Lys Met Leu Lys Ala Tyr Asp Phe Phe Tyr Gly Asn Val Glu Gly Ser
195 200 205

Asp Ile Phe Lys Gly Val Val Asp Val Val Val Cys Asp Gly Phe Met
210 215 220

Gly Asn Val Val Leu Lys Thr Thr Glu Gly Val Ala Ser Ala Ile Gly
225 230 235 240

Ser Ile Phe Lys Asp Glu Ile Lys Ser Ser Phe Lys Ser Lys Met Gly
245 250 255

Ala Leu Met Leu Lys Asn Ala Phe Asp Ile Leu Lys Gln Lys Thr Asp
260 265 270

Tyr Ala Glu Tyr Gly Gly Ala Pro Leu Leu Gly Val Asn Lys Ser Val
275 280 285

Ile Ile Ser His Gly Lys Ser Asn Ala Arg Ala Ile Glu Cys Ala Ile
290 295 300

Tyr Gln Ala Ile Ser Ala Val Glu Ser Gln Val Cys Leu Arg Ile Thr
305 310 315 320

Gln Ala Phe Glu Ser Leu Lys Pro Ser Val Ser Gln Ser Asp Gln Gln
325 330 335

Asp Ala

<210> 199

<211> 331

<212> PRT

<213> Helicobacter pylori

<400> 199

Met Glu Phe Tyr Ala Ser Leu Lys Ser Ile Ala Met His Val Pro Ser
1 5 10 15

Glu Arg Val Lys Asn Ala Glu Phe Gln Gln Phe Leu Asp Thr Ser Asp
20 25 30

Glu Trp Ile Glu Lys Arg Thr Gly Ile Lys Glu Arg Arg Phe Ala Asn
35 40 45

Asp Glu Glu Lys Ser Ser Asp Leu Gly Val Ile Ala Ala Lys Gln Ala
50 55 60

Ile Glu Arg Ala His Leu Thr Pro Lys Asp Ile Asp Leu Val Val Val
65 70 75 80

Ala Thr Leu Ser Pro Asp Phe Leu Ala Met Pro Ser Thr Ala Cys Val
85 90 95

Leu Ser Ala Lys Leu Gly Ile Glu Asn Lys Pro Ala Phe Asp Ile Ser
100 105 110

Ala Ala Cys Thr Gly Phe Ile Tyr Leu Leu Ser Val Ala Lys Ala Tyr
115 120 125

Val Glu Ser Gly Met Tyr Glu Asn Val Leu Ile Val Gly Ala Glu Lys
130 135 140

Thr Ser Ser Val Leu Asp Phe Lys Asp Arg Gly Thr Cys Ile Leu Phe
145 150 155 160

Gly Asp Gly Ala Gly Ala Cys Val Ile Gly Arg Thr Lys Arg Leu Lys
165 170 175

Glu Ser Ile Leu Asp Val Gln Ile Ser Ala Asn Gly Asn Phe Ser Asn
180 185 190

Tyr Leu Tyr Thr Pro Arg Thr Leu Lys Pro Thr Pro Phe Asn Ala Lys
195 200 205

Glu Glu Ala Ser Glu Pro Phe Leu Cys Met Lys Gly Asn Glu Val Phe
210 215 220

Lys Leu Ala Val Lys Thr Leu Leu Lys Asp Val Glu Met Ile Leu Glu
225 230 235 240

Lys Asn Ala Leu Lys Pro Glu Asp Val Arg Leu Phe Ile Pro His Gln
245 250 255

Ala Asn Phe Arg Ile Ile Gln Ala Val Arg Glu His Leu Asp Phe Lys
260 265 270

Asp Glu Gln Val Val Leu Thr Val His Lys Tyr Gly Asn Thr Ser Ala
275 280 285

Ala Ser Ile Pro Met Ala Met Gly Glu Ala Tyr Glu Glu Gly Arg Leu
290 295 300

Lys Lys Gly Asp Leu Met Leu Leu Asp Ala Phe Gly Gly Gly Leu Thr
305 310 315 320

Trp Gly Ser Ala Leu Val Tyr Phe Gly Gly Ser
325 330

<210> 200

<211> 621

<212> PRT

<213> Helicobacter pylori

<400> 200

Met Ser Asn Gln Glu Tyr Thr Phe Gln Thr Glu Ile Asn Gln Leu Leu
1 5 10 15

Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu Ile Phe Leu Arg
20 25 30

Glu Leu Val Ser Asn Ala Ser Asp Ala Leu Asp Lys Leu Asn Tyr Leu
35 40 45

Met Leu Thr Asp Glu Lys Leu Lys Gly Leu Asn Thr Thr Pro Ser Ile
50 55 60

His Leu Ser Phe Asp Ser Gln Lys Lys Thr Leu Thr Ile Lys Asp Asn
65 70 75 80

Gly Ile Gly Met Asp Lys Asn Asp Leu Ile Glu His Leu Gly Thr Ile
85 90 95

Ala Lys Ser Gly Thr Lys Asn Phe Leu Ser Ala Leu Ser Gly Asp Lys
100 105 110

Lys Lys Asp Ser Ala Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
115 120 125

Ala Phe Met Val Ala Ser Lys Ile Val Val Gln Thr Lys Lys Val Asn
130 135 140

Ser Asp Gln Ala Tyr Ala Trp Val Ser Asp Gly Lys Gly Lys Phe Glu
145 150 155 160

Ile Ser Glu Cys Val Lys Asp Glu Gln Gly Thr Glu Ile Thr Leu Phe
165 170 175

Leu Lys Asp Glu Asp Ser His Phe Ala Ser Arg Trp Glu Ile Asp Ser
180 185 190

Val Val Lys Lys Tyr Ser Glu His Ile Pro Phe Pro Ile Phe Leu Thr
195 200 205

Tyr Thr Asp Thr Lys His Glu Gly Glu Gly Asp Asn Gln Lys Glu Ile
210 215 220

Lys Glu Glu Lys Cys Glu Gln Ile Asn Gln Ala Ser Ala Leu Trp Lys
225 230 235 240

Met Asn Lys Ser Glu Leu Lys Asp Lys Asp Tyr Lys Glu Phe Tyr Gln
245 250 255

Ser Phe Ala His Asp Asn Ser Glu Pro Leu Ser Tyr Ile His Asn Lys
260 265 270

Val Glu Gly Ser Leu Glu Tyr Thr Thr Leu Phe Tyr Ile Pro Ser Thr
275 280 285

Ala Pro Phe Asp Met Phe Arg Val Asp Tyr Lys Ser Gly Val Lys Leu
290 295 300

Tyr Val Lys Arg Val Phe Ile Thr Asp Asp Asp Lys Glu Leu Leu Pro
305 310 315 320

Ser Tyr Leu Arg Phe Val Lys Gly Val Ile Asp Ser Glu Asp Leu Pro
325 330 335

Leu Asn Val Ser Arg Glu Ile Leu Gln Gln Asn Lys Ile Leu Ala Asn
340 345 350

Ile Arg Ser Ala Ser Val Lys Lys Ile Leu Ser Glu Ile Glu Arg Leu
355 360 365

Ser Lys Asp Glu Lys Asn Tyr His Lys Phe Tyr Glu Pro Phe Gly Lys
370 375 380

Val Leu Lys Glu Gly Leu Tyr Gly Asp Phe Glu Asn Lys Glu Lys Leu
385   390   395   400

Leu Glu Leu Leu Arg Phe Tyr Ser Lys Asp Lys Glu Lys Leu Ile Ser
            405   410   415

Leu Lys Glu Tyr Lys Glu Asn Leu Lys Glu Asn Gln Lys Ser Ile Tyr
        420   425   430

Tyr Leu Leu Gly Glu Asn Leu Asp Leu Leu Lys Ala Ser Pro Leu Leu
    435   440   445

Glu Lys Tyr Ala Gln Lys Gly Tyr Asp Val Leu Leu Leu Ser Asp Glu
450   455   460

Ile Asp Ala Phe Val Met Pro Gly Val Asn Glu Tyr Asp Lys Thr Pro
465   470   475   480

Phe Lys Asp Ala Ser His Ser Glu Ser Leu Lys Glu Leu Gly Leu Glu
            485   490   495

Glu Ile His Asp Glu Val Lys Asp Gln Phe Lys Asp Leu Met Lys Ala
        500   505   510

Phe Glu Glu Asn Leu Lys Asp Glu Ile Lys Gly Val Glu Leu Ser Ser
    515   520   525

His Leu Thr Ser Ala Val Ala Leu Ile Gly Asp Glu Gln Asn Ala Met
530   535   540

Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser Lys
545   550   555   560

Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu
            565   570   575

Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr
        580   585   590

Asp Gly Ala Lys Leu Leu Glu Lys Gly Ala Leu Lys Asp Ala Lys Ser
    595   600   605

Phe Asn Glu Arg Leu Asn Ser Val Leu Leu Lys Ala Leu
610   615   620

<210> 201

<211> 250

<212> PRT

<213> Helicobacter pylori

<400> 201

Met Leu Gly Asn Val Lys Lys Thr Leu Phe Gly Val Leu Cys Leu Gly
1 5 10 15

Thr Leu Cys Leu Arg Gly Leu Met Ala Glu Pro Asp Ala Lys Glu Leu
20 25 30

Val Asn Leu Gly Ile Glu Ser Ala Lys Lys Gln Asp Phe Ala Gln Ala
35 40 45

Lys Thr His Phe Glu Lys Ala Cys Glu Leu Lys Asn Gly Phe Gly Cys
50 55 60

Val Phe Leu Gly Ala Phe Tyr Glu Glu Gly Lys Gly Val Gly Lys Asp
65 70 75 80

Leu Lys Lys Ala Ile Gln Phe Tyr Thr Lys Gly Cys Glu Leu Asn Asp
85 90 95

Gly Tyr Gly Cys Asn Leu Leu Gly Asn Leu Tyr Tyr Asn Gly Gln Gly
100 105 110

Val Ser Lys Asp Ala Lys Lys Ala Ser Gln Tyr Tyr Ser Lys Ala Cys
115 120 125

Asp Leu Asn His Ala Glu Gly Cys Met Val Leu Gly Ser Leu His His
130 135 140

Tyr Gly Val Gly Thr Pro Lys Asp Leu Arg Lys Ala Leu Asp Leu Tyr
145 150 155 160

Glu Lys Ala Cys Asp Leu Lys Asp Ser Pro Gly Cys Ile Asn Ala Gly
165 170 175

Tyr Ile Tyr Ser Val Thr Lys Asn Phe Lys Glu Ala Ile Val Arg Tyr
180 185 190

Ser Lys Ala Cys Glu Leu Lys Asp Gly Arg Gly Cys Tyr Asn Leu Gly
195 200 205

Val Met Gln Tyr Asn Ala Gln Gly Thr Ala Lys Asp Glu Lys Gln Ala
210 215 220

Val Glu Asn Phe Lys Lys Gly Cys Lys Ser Ser Val Lys Glu Ala Cys
225 230 235 240

Asp Ala Leu Lys Glu Leu Lys Ile Glu Leu
245 250

<210> 202

<211> 390

<212> PRT

<213> Helicobacter pylori

<400> 202

Met Arg Lys Lys Gly Met Phe Glu Lys Ile Gln Lys Glu Trp Leu Ser
1 5 10 15

Asn Ile Gln Lys Asp Leu Leu Ser Gly Phe Val Val Gly Leu Ser Val
20 25 30

Ile Pro Glu Thr Ala Gly Phe Ala Ile Met Val Gly Leu Asp Val Gly
35 40 45

Val Ala Phe Tyr Thr Thr Phe Tyr Met Ala Phe Val Leu Ser Leu Phe
50 55 60

Gly Ala Arg Lys Ala Met Ile Ser Ala Ala Ala Gly Ser Val Ala Leu
65 70 75 80

Ile Leu Val Gly Val Val Lys Asn Tyr Gly Leu Glu Tyr Ala Gly Val
85 90 95

Ala Thr Leu Met Ala Gly Val Leu Gln Ile Leu Leu Gly Tyr Leu Lys
100 105 110

Ile Gly Asn Leu Leu Arg Phe Ile Pro Gln Ser Val Met Tyr Gly Phe
115 120 125

Val Asn Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu
130 135 140

Gln Asn Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu
145 150 155 160

Ile Ile Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu
165 170 175

Ile Cys Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His
180 185 190

Ala Pro Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe
195 200 205

Ile Ile Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu
210 215 220

Pro Tyr Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu
225 230 235 240

Thr Ala Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys
245 250 255

Asn Lys Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu
260 265 270

Leu Gly Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn
275 280 285

Ala Lys Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe
290 295 300

Ser Leu Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile
305 310 315 320

Pro Ile Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr
325 330 335

Phe Asn Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp
340 345 350

Thr Leu Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn
355 360 365

Leu Ala Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile
370 375 380

Lys Ser Lys Gly Ile Ala
385 390

<210> 203

<211> 483

<212> PRT

<213> Helicobacter pylori

<400> 203

Met Lys Lys Thr Ile Leu Leu Ser Leu Met Val Ser Ser Leu Leu Ala
1 5 10 15

Glu Asn Asp Gly Val Phe Met Ser Val Gly Tyr Gln Ile Gly Glu Ala
20 25 30

Val Gln Gln Val Lys Asn Thr Gly Glu Ile Gln Lys Val Ser Asn Ala
35 40 45

Tyr Glu Asn Leu Asn Asn Leu Leu Thr Arg Tyr Asn Glu Leu Lys Gln
    50   55   60

Thr Ala Ser Asn Thr Asn Ser Ser Thr Ala Gln Ala Ile Asp Asn Leu
65   70   75   80

Lys Glu Ser Ala Ser Arg Leu Lys Thr Thr Pro Asn Ser Ala Asn Gln
                85   90   95

Ala Val Ser Ser Ala Leu Ser Ser Ala Val Ala Met Trp Gln Val Ile
            100   105   110

Val Ser Asn Leu Ala Asn Asn Ser Leu Pro Thr Ser Glu Tyr Asn Lys
        115   120   125

Ile Asn Ala Ile Ser Gln Ser Leu Gln Asn Thr Leu Glu Asn Lys Asn
    130   135   140

Asn Asp Leu Lys Ile Glu Asn Asp Tyr Asp His Leu Leu Thr Gln Ala
145   150   155   160

Ser Thr Ile Ile Asn Thr Leu Gln Ser Gln Cys Pro Gly Ile Asp Gly
                165   170   175

Gly Asn Gly Lys Pro Trp Gly Ile Asn Ala Ser Gly Asn Ala Cys Asn
            180   185   190

Ile Phe Gly Asn Thr Phe Asn Ala Ile Thr Ser Met Ile Asp Ser Ala
        195   200   205

Lys Lys Ala Ala Ala Asp Ala Arg Arg Thr Ala Pro Glu Ser Pro Asn
    210   215   220

Gln Pro Ser Ala Phe Asn Asn Ala Asp Phe Asn Lys Asn Leu Asn Gln
225   230   235   240

Val Ser Ser Val Ile Asn Asp Thr Ile Ser Tyr Leu Lys Gly Asp Asn
                245   250   255

Leu Ala Thr Ile Tyr Asn Thr Leu Gln Lys Thr Pro Asp Ser Lys Gly
            260   265   270

Phe Gln Ser Leu Val Ser Arg Ser Ser Tyr Ser Tyr Ser Leu Asn Glu
        275   280   285

Thr Gln Tyr Ser Glu Phe Gln Thr Thr Thr Lys Glu Phe Gly His Asn
    290   295   300

Pro Phe Arg Ser Val Gly Leu Ile Asn Ser Gln Ser Asn Asn Gly Ala
305   310   315   320

Met Asn Gly Val Gly Val Gln Leu Gly Tyr Lys Gln Phe Phe Gly Lys
325 330 335

Asn Lys Phe Phe Gly Ile Arg Tyr Tyr Ala Phe Phe Asp Tyr Asn His
340 345 350

Ala Tyr Ile Lys Ser Asn Phe Phe Asn Ser Ala Ser Asn Val Phe Thr
355 360 365

Tyr Gly Ala Gly Ser Asp Leu Leu Leu Asn Phe Ile Asn Gly Gly Ser
370 375 380

Asp Lys Asn Arg Lys Val Ser Phe Gly Ile Phe Gly Gly Ile Ala Leu
385 390 395 400

Ala Gly Thr Thr Trp Leu Asn Ser Gln Phe Met Asn Leu Lys Thr Thr
405 410 415

Asn Ser Ala Tyr Ser Ala Lys Ile Asn Asn Thr Asn Phe Gln Phe Leu
420 425 430

Phe Asn Thr Gly Leu Arg Leu Gln Gly Ile His His Gly Val Glu Leu
435 440 445

Gly Val Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser Phe Met Gly
450 455 460

Ala Lys Leu Ala Tyr Arg Arg Leu Tyr Ser Val Tyr Phe Asn Tyr Val
465 470 475 480

Leu Ala Tyr

<210> 204

<211> 355

<212> PRT

<213> Helicobacter pylori

<400> 204

Met Gly Val Lys Phe Leu Lys Ile Leu Val Cys Gly Leu Phe Phe Trp
1 5 10 15

Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
20 25 30

Val Ala Glu Lys Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Thr Ser
35 40 45

Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
50 55 60

Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
65 70 75 80

Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
85 90 95

Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Thr
100 105 110

Gln Asn Tyr Gln Glu Ala Ile Asp Ala Tyr Ala Lys Ala Cys Val Leu
115 120 125

Lys His Pro Glu Ser Cys Tyr Asn Leu Gly Ile Ile Tyr Asp Arg Lys
130 135 140

Ile Lys Gly Asn Ala Asp Gln Ala Val Thr Tyr Tyr Gln Lys Ser Cys
145 150 155 160

Asn Phe Asp Met Ala Lys Gly Cys Tyr Val Leu Gly Val Ala Tyr Glu
165 170 175

Lys Gly Phe Leu Glu Val Lys Gln Ser Asn His Lys Ala Val Ile Tyr
180 185 190

Tyr Leu Lys Ala Cys Arg Leu Asp Asp Gly Gln Ala Cys Arg Ala Leu
195 200 205

Gly Ser Leu Phe Glu Asn Gly Asp Ala Gly Leu Asp Glu Asp Phe Glu
210 215 220

Val Ala Phe Asp Tyr Leu Gln Lys Ala Cys Gly Leu Asn Asn Ser Gly
225 230 235 240

Gly Cys Ala Ser Leu Gly Ser Met Tyr Met Leu Gly Arg Tyr Val Lys
245 250 255

Lys Asp Pro Gln Lys Ala Phe Asn Phe Phe Lys Gln Ala Cys Asp Met
260 265 270

Gly Ser Ala Val Ser Cys Ser Arg Met Gly Phe Met Tyr Ser Gln Gly
275 280 285

Asp Ala Val Pro Lys Asp Leu Arg Lys Ala Leu Asp Asn Tyr Glu Arg
290 295 300

Gly Cys Asp Met Gly Asp Glu Val Gly Cys Phe Ala Leu Ala Gly Met
305 310 315 320

Tyr Tyr Asn Met Lys Asp Lys Glu Asn Ala Ile Met Ile Tyr Asp Lys
325 330 335

Gly Cys Lys Leu Gly Met Lys Gln Ala Cys Glu Asn Leu Thr Lys Leu
340 345 350

Arg Gly Tyr
355

<210> 205

<211> 449

<212> PRT

<213> Helicobacter pylori

<400> 205

Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr Leu Ala Phe Thr
1 5 10 15

His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu Ala Ile Asn Ser
20 25 30

Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys Asn His Cys Pro
35 40 45

Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn Arg Phe Glu Ile
50 55 60

Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu Gln Lys Asn Ala
65 70 75 80

Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser Val Ser Asp Leu
85 90 95

Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala Val His His Val
100 105 110

Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val Gly Glu Thr Gln
115 120 125

Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala Phe Glu Glu Lys
130 135 140

Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe Ala Phe Lys Cys
145 150 155 160

Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys Gln Gly Val Ser
165 170 175

Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile Phe Glu Lys Glu
180 185 190

Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu Gly Glu Met Ala
195 200 205

Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe Glu Ala Leu Ile
210 215 220

Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile Lys Glu Leu Glu
225 230 235 240

Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn Leu Asn Ala Tyr
245 250 255

Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser Ser Pro His Phe
260 265 270

Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe Arg Arg Phe Trp
275 280 285

Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro Val Leu Asp Asn
290 295 300

Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met Val Arg Glu Asn
305 310 315 320

Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr Glu Ile Val Gly
325 330 335

Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser Leu Glu Val Glu
340 345 350

Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile Ser Ala Gln Lys
355 360 365

Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro Lys Glu Tyr Glu
370 375 380

Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn Thr Phe Leu His
385 390 395 400

Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys Glu Glu Ser Asp
405 410 415

Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu Asp Lys Ser Asn
420 425 430

Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys Glu Tyr Tyr Glu
435 440 445

Glu

<210> 206

<211> 348

<212> PRT

<213> Helicobacter pylori

<400> 206

Met Phe Ile Val Ala Val Leu Met Leu Ala Phe Leu Ile Phe Val His
1 5 10 15

Glu Leu Gly His Phe Thr Ile Ala Arg Ile Cys Gly Val Lys Val Glu
20 25 30

Val Phe Ser Ile Gly Phe Gly Lys Lys Leu Cys Phe Phe Lys Leu Phe
35 40 45

Gly Thr Gln Phe Ala Leu Ser Leu Ile Pro Leu Gly Gly Tyr Val Lys
50 55 60

Leu Lys Gly Met Asp Lys Glu Glu Asn Gly Met Asn Glu Thr Thr Asp
65 70 75 80

Asp Ser Tyr Ala Gln Lys Ser Pro Phe Gln Lys Leu Trp Ile Leu Phe
85 90 95

Gly Gly Ala Phe Phe Asn Phe Leu Phe Ala Ile Leu Val Tyr Phe Phe
100 105 110

Leu Ala Leu Gly Gly Glu Lys Val Leu Leu Pro Val Ile Gly Asp Leu
115 120 125

Asp Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly Asp Lys Ile Leu
130 135 140

Ser Ile Asn His Lys Lys Ile Ala Ser Phe Arg Glu Ile Arg Ser Val
145 150 155 160

Val Ala Arg Ala Arg Gly Glu Leu Val Leu Glu Ile Glu Arg Asn His
165 170 175

Gln Val Leu Glu Lys Arg Leu Thr Pro Lys Ile Val Ala Val Ile Ser
180 185 190

Asp Ser Asn Asp Pro Asn Glu Met Ile Arg Tyr Lys Ala Ile Gly Ile
195 200 205

Lys Pro Asp Met Gln Lys Met Gly Val Val Ser Tyr Ser Leu Phe Gln
210 215 220

Ala Phe Glu Lys Ala Leu Ser Arg Phe Lys Glu Gly Val Val Leu Ile
225 230 235 240

Val Asp Ser Leu Arg Arg Leu Ile Met Gly Ser Ser Ser Val Lys Glu
245 250 255

Leu Ser Gly Val Val Gly Ile Val Gly Ala Leu Ser His Ala Asn Ser
260 265 270

Leu Ser Met Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu Gly
275 280 285

Ile Leu Asn Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met Leu
290 295 300

Gly Val Val Phe Lys Asn Ile Phe His Ile Thr Leu Pro Thr Pro Ile
305 310 315 320

Gln Asn Ala Leu Trp Leu Ala Gly Val Gly Phe Leu Val Phe Ile Met
325 330 335

Phe Leu Gly Leu Phe Asn Asp Leu Thr Arg Leu Leu
340 345

<210> 207

<211> 378

<212> PRT

<213> Helicobacter pylori

<400> 207

Met Leu Leu Lys Asn Ala Ser Phe Tyr Asp Asp Glu Val Leu Lys Arg
1 5 10 15

Ala Asp Ile Arg Leu Lys Asp Ser Leu Ile Thr Glu Ile Lys Glu Asn
20 25 30

Leu Ser Pro Ile Asn Asn Glu Glu Val Ile Glu Cys Arg Asp Leu Phe
35 40 45

Val Leu Pro Ser Phe Ile Asp Leu Ser Val Thr Gly Leu Glu Gly Tyr
50 55 60

Glu Asn Leu Lys Gln Lys Ala Phe Lys Gly Gly Val Gly Leu Leu Asn
65 70 75 80

Val Phe Asn Cys Asp Gln Ser Gly Ile Lys Asn Ile Met Ala Ile Lys
85 90 95

Asn Asn Gln Leu Ala Asp Ile Ala Thr Leu Lys Asn Lys Gly Gly Glu
100 105 110

Ile Leu Ile Ala Pro Ser Asp Ala Phe Leu Glu Leu Ile Ser His Tyr
115 120 125

Ala Lys Ser Tyr Asn Leu Pro Leu Leu Ile Ser Leu Glu Asn Ser Phe
130 135 140

Glu Ala Leu Asn Ser Gly Glu Leu Ala Tyr Glu Leu Gly Gln Asn Phe
145 150 155 160

Val Glu Asn Ala Phe Glu Asn Thr Arg Leu Val Arg Phe Met Glu Val
165 170 175

Ser Arg Ala Leu Gln Ile Pro Val Leu Leu Asp Lys Val Asn Ser Ile
180 185 190

Thr Thr Leu Lys Leu Ile Lys Ala Phe Asn Asp Leu Gly Ala Lys Leu
195 200 205

Gln Ala Gln Thr Pro Leu Ser His Leu Val Leu Asp Glu Ser Val Tyr
210 215 220

Glu Asp Tyr Glu Pro Arg Phe Lys Ile Ala Pro Pro Leu Arg Asp Lys
225 230 235 240

Glu Ser Gln Asn Ala Leu Lys Glu Ala Leu Lys Asn Asn Glu Ile Ala
245 250 255

Met Leu Thr Ser Leu His Ala Ser Lys Asn Ser Asn Ala Gln Leu Phe
260 265 270

Glu Glu Ser Ala Phe Gly Cys Glu Ser Ile Glu Asp Ala Phe Ser Val
275 280 285

Ala Tyr Thr Phe Leu Val Gln Lys Lys Val Ile Ser Phe Gln Gln Leu
290 295 300

Ile Lys Val Met Ala Ile Asn Gln Ala Lys Phe Leu Lys Leu Asn Ala
305 310 315 320

Gly Glu Val Lys Glu Asn Gln Leu Ala Asn Leu Met Ile Val Asp Leu
325 330 335

Asn Ala Gln Thr Arg Val Ser Asn Gln Asn Ser Pro Phe Tyr Gly Leu
340 345 350

Glu Leu Tyr Gly Glu Val Gln Arg Met Ile Leu Lys Gly Gln Thr Thr
355 360 365

Phe Ile Lys Glu Asn Ala Cys Lys Lys Ser
370 375

<210> 208

<211> 340

<212> PRT

<213> Helicobacter pylori

<400> 208

Leu Lys Ile Ala Ile Val Arg Leu Ser Ala Leu Gly Asp Ile Ile Val
1 5 10 15

Ser Ala Val Phe Leu Ala Val Ile Lys Glu Cys Leu Pro Asn Ala Gln
20 25 30

Ile Glu Trp Phe Val Asp Glu Arg Phe Ser Ala Ile Leu Glu His Ser
35 40 45

Pro Tyr Ile Asp Lys Leu His Pro Ile Ala Leu Lys Ser Ala Leu Lys
50 55 60

Thr Leu Asn Pro Leu Lys Ile Phe Lys Leu Phe Lys Ser Leu Arg Ala
65 70 75 80

Tyr Glu Tyr Asp Ile Ile Ile Asp Met Gln Gly Leu Val Lys Ser Ala
85 90 95

Leu Ile Thr Gln Met Leu Lys Ala Pro Lys Lys Val Gly Phe Asp Tyr
100 105 110

Ala Ser Ala Arg Glu Gly Leu Ser Met Phe Phe Tyr Ser Gln Lys Val
115 120 125

Ser Ile Ala Tyr Asp Glu Pro Val Leu Lys Arg Asn Phe Thr Leu Leu
130 135 140

Ser His Ala Leu Asn Leu Pro Gln Lys Glu Ile Ser Lys Glu Ile Ser
145 150 155 160

Glu Ser Leu Ser Ser Arg Ala Lys Ala Phe Ser Tyr Gln Pro Ser Pro
165 170 175

Lys Ile Asp Ala Leu Asn Leu Asn Lys Asn Lys Pro Lys Ile Leu Phe
180 185 190

Ile Leu Glu Thr Ser Lys Ile Asn Lys Thr Tyr Pro Ile Glu Arg Phe
195 200 205

Lys Glu Leu Ala Leu Ile Leu Glu Asn Phe Gln Ile Cys Leu Leu Trp
210 215 220

His Ala Asp Glu Tyr Lys Ala Thr Thr Leu Tyr His Ala Leu Lys His
225 230 235 240

Gln Arg Asp Val Leu Leu Leu Pro Lys Leu Thr Leu Asn Glu Val Lys
245 250 255

Ala Leu Leu Phe Lys Met Asp Leu Ile Ile Gly Gly Asp Thr Gly Ile
260 265 270

Thr His Leu Ala Trp Ala Leu Gln Lys Pro Ser Ile Thr Leu Tyr Gly
275 280 285

Asn Thr Pro Met Glu Arg Phe Lys Leu Glu Ser Pro Ile Asn Val Ser
290 295 300

Leu Thr Gly Asn Ser Asn Ala Asn Tyr His Lys Lys Asp Phe Ser Ile
305 310 315 320

Gln Asn Ile Glu Pro Lys Lys Ile Lys Glu Cys Val Leu Asn Ile Leu
325 330 335

Lys Glu Lys Glu
340

<210> 209

<211> 2893

<212> PRT

<213> Helicobacter pylori

<400> 209

Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys Arg Ser His Gln
1 5 10 15

Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu
20 25 30

Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn Leu Trp Asp Leu
35 40 45

Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp Val Lys Gly Ser
50 55 60

Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu Lys Asn Val Trp
65   70   75   80

Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala Ala Asn Tyr Leu
                85   90   95

Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser Gly Asn Glu Thr
            100   105   110

Gly Thr Tyr Ser Leu Ser Gly Phe Thr Asn Tyr Val Gly Gly Asn Leu
        115   120   125

Thr Ile Asn Leu Gly Asn Ser Val Val Leu Asp Leu Ser Gly Ser Asn
    130   135   140

Ser Phe Thr Ser Tyr Gln Gly Tyr Asn Gln Gly Lys Asp Asp Val Thr
145   150   155   160

Phe Thr Val Gly Ala Ile Asn Leu Asn Gly Thr Leu Glu Val Gly Asn
                165   170   175

Arg Val Gly Ser Gly Ala Gly Thr His Thr Gly Thr Ala Thr Leu Asn
            180   185   190

Leu Asn Ala Asn Lys Val Asn Ile Asn Ser Asn Ile Asn Ala Tyr Lys
        195   200   205

Thr Ser Gln Val Asn Ile Gly Asn Ala Asn Ser Val Ile Thr Ile Gly
    210   215   220

Ser Val Ser Leu Ser Gly Asp Val Cys Ser Ser Leu Ala Ser Val Gly
225   230   235   240

Ile Gly Ala Asn Cys Ser Thr Ser Gly Pro Ser Tyr Ser Phe Lys Gly
                245   250   255

Thr Thr Asn Ala Thr Asn Thr Ala Phe Ser Asn Ala Ser Gly Ser Phe
            260   265   270

Thr Phe Glu Glu Asn Ala Thr Phe Ser Gly Ala Lys Trp Asn Gly Gly
        275   280   285

Thr Tyr Thr Phe Asn Lys Glu Phe Ser Ala Thr Asn Asn Thr Ala Phe
    290   295   300

Ser Ser Gly Ser Phe Asn Phe Lys Gly Val Ser Ser Phe Asn Gly Thr
305   310   315   320

Ser Phe Ser Asn Ala Ser Tyr Thr Phe Asp Asn Gln Ala Thr Phe Gln
                325   330   335

Asn Ser Ser Phe Asn Gly Gly Thr Phe Thr Phe Asn Asn Gln Thr Asn
340 345 350

Pro Thr Asn Asn Ala Gln His Pro Gln Ile Gln Asn Ser Ser Phe Ser
355 360 365

Gly Asn Ala Thr Thr Leu Lys Gly Phe Val Asn Phe Gln Gln Ala Phe
370 375 380

Asn Asn Ser Asn His Gln Leu Thr Ile Gln Asn Ala Ser Phe Asn Asn
385 390 395 400

Ala Thr Phe Asn Asn Thr Gly Lys Ile Thr Ile Glu Lys Asp Ala Ser
405 410 415

Phe Asn Asn Thr Thr Phe Asn Thr Ser Val Asp Thr Asn Asn Met Ser
420 425 430

Val Thr Gly Gly Val Thr Leu Ser Gly Lys Asn Asp Leu Lys Asn Gly
435 440 445

Ser Thr Leu Asp Phe Gly Ser Ser Lys Ile Thr Leu Ala Gln Gly Thr
450 455 460

Thr Phe Asn Leu Thr Ser Leu Gly Ser Glu Lys Ser Val Thr Ile Leu
465 470 475 480

Asn Ser Ser Gly Gly Ile Thr Tyr Ser Asn Leu Leu Asn His Ala Ile
485 490 495

Asn Gly Leu Thr Ser Ala Leu Lys Thr Asn Glu Ser Leu Ser Asn Pro
500 505 510

Gln Ser Phe Ala Gln Gly Leu Trp Asp Ile Ile Thr Tyr Asn Gly Val
515 520 525

Thr Gly Gln Leu Leu Asn Glu Asn Ala Ala Thr Ser Lys Pro Thr Asp
530 535 540

Ser Ser Pro Ser Lys Ser Ser Thr Asn Ser Thr Gln Val Tyr Gln Val
545 550 555 560

Gly Tyr Lys Ile Gly Asp Thr Ile Tyr Lys Leu Gln Glu Thr Phe Ser
565 570 575

His Asn Ser Ile Ile Ile Gln Ala Leu Glu Ser Gly Thr Tyr Thr Pro
580 585 590

Pro Pro Val Ile Asn Gly Ser Lys Phe Asp Leu Ser Ala Ser Asn Tyr
595 600 605

Ile Asn Ala Asp Met Pro Trp Tyr Asp His Lys Tyr Tyr Ile Pro Lys
    610   615   620

Ser Gln Asn Phe Thr Glu Ser Gly Thr Tyr Tyr Leu Pro Ser Val Gln
625   630   635   640

Ile Trp Gly Ser Tyr Thr Asn Ser Phe Lys Gln Thr Phe Ser Ala Asn
                645   650   655

Gly Ser Asn Leu Val Ile Gly Tyr Asn Ser Thr Trp Thr Asp His Asn
            660   665   670

Val Ser Ser Ser Gly Thr Val Ser Phe Gly Asp Thr Ser Gly Ser Ala
        675   680   685

Leu Asn Gly His Cys Gly Pro Trp Pro Tyr Tyr Gln Cys Thr Gly Thr
    690   695   700

Thr Asn Gly Thr Tyr Ser Ala Tyr His Val Tyr Ile Thr Ala Asn Leu
705   710   715   720

Arg Ser Gly Asn Arg Ile Gly Thr Gly Gly Ala Ala Asn Leu Ile Phe
                725   730   735

Asn Gly Val Asp Ser Ile Asn Ile Ala Asn Ala Thr Ile Thr Gln His
            740   745   750

Asn Ala Gly Ile Tyr Ser Ser Ser Met Thr Phe Ser Thr Gln Ser Met
        755   760   765

Asp Asn Ser Gln Asn Leu Asn Gly Leu Asn Ser Asn Gly Lys Leu Ser
    770   775   780

Val Tyr Gly Thr Thr Phe Thr Asn Glu Ala Lys Asp Gly Lys Phe Ile
785   790   795   800

Phe Asn Ala Gly Gln Ala Val Phe Glu Asn Thr Asn Phe Asn Gly Gly
                805   810   815

Ser Tyr Gln Phe Ser Gly Asp Ser Leu Asn Phe Ser Asn Asn Asn Gln
            820   825   830

Phe Asn Ser Gly Ser Phe Glu Ile Ser Ala Lys Asn Ala Ser Phe Asn
        835   840   845

Asn Ala Asn Phe Asn Asn Ser Ala Ser Phe Asn Phe Asn Asn Ser Asn
    850   855   860

Ala Thr Thr Ser Phe Val Gly Asp Phe Thr Asn Ala Asn Ser Asn Leu
865   870   875   880

Gln Ile Ala Gly Asn Ala Val Phe Gly Asn Ser Thr Asn Gly Ser Gln
885 890 895

Asn Thr Ala Asn Phe Asn Asn Thr Gly Ser Val Asn Ile Ser Gly Asn
900 905 910

Ala Thr Phe Asp Asn Val Val Phe Asn Gly Pro Thr Asn Thr Ser Val
915 920 925

Lys Gly Gln Val Thr Leu Asn Asn Ile Thr Leu Lys Asn Leu Asn Ala
930 935 940

Pro Leu Ser Phe Gly Asp Gly Thr Ile Thr Phe Asn Ala His Ser Val
945 950 955 960

Ile Asn Ile Ala Glu Ser Ile Thr Asn Gly Asn Pro Ile Thr Leu Val
965 970 975

Ser Ser Ser Lys Glu Ile Glu Tyr Asn Asn Ala Phe Ser Lys Asn Leu
980 985 990

Trp Gln Leu Ile Asn Tyr Gln Gly His Gly Ala Ser Ser Glu Lys Leu
995 1000 1005

Val Ser Ser Ala Gly Asn Gly Val Tyr Asp Val Val Tyr Ser Phe
1010 1015 1020

Asn Asn Gln Thr Tyr Asn Phe Gln Glu Val Phe Ser Gln Asn Ser
1025 1030 1035

Ile Ser Ile Arg Arg Leu Gly Val Asn Met Val Phe Asp Tyr Val
1040 1045 1050

Asp Met Glu Lys Ser Asp His Leu Tyr Tyr Gln Asn Ala Leu Gly
1055 1060 1065

Phe Met Thr Tyr Met Pro Asn Ser Tyr Asn Asn Asn Leu Gly Asn
1070 1075 1080

Ala Asn Asn Thr Ile Tyr Tyr Tyr Asp Lys Ser Ile Asp Phe Tyr
1085 1090 1095

Ala Ser Gly Lys Thr Leu Phe Thr Lys Ala Glu Phe Ser Gln Thr
1100 1105 1110

Phe Thr Gly Gln Asn Ser Ala Ile Val Phe Gly Ala Lys Ser Ile
1115 1120 1125

Trp Thr Ser Leu Ser Asp Ala Pro Gln Ser Asn Thr Ile Ile Arg
1130 1135 1140

Phe Gly Asp Asn Lys Gly Ala Gly Ser Asn Asp Ala Ser Gly His
1145 1150 1155

Cys Trp Asn Leu Gln Cys Ile Gly Phe Ile Thr Gly His Tyr Glu
1160 1165 1170

Ala Gln Lys Ile Tyr Ile Thr Gly Ser Ile Glu Ser Gly Asn Arg
1175 1180 1185

Ile Ser Ser Gly Gly Gly Ala Ser Leu Asn Phe Asn Gly Leu Gln
1190 1195 1200

Gly Ile Leu Leu Thr Asn Ala Thr Leu Tyr Asn Arg Ala Ala Gly
1205 1210 1215

Thr Gln Ser Ser Ser Met Asn Phe Ile Ser Asn Ser Ala Asn Ile
1220 1225 1230

Gln Ala Gln Asn Ser Tyr Phe Ile Asp Asp Thr Ala Gln Asn Gly
1235 1240 1245

Gly Asn Pro Asn Phe Ser Phe Asn Ala Leu Asn Leu Asp Phe Ser
1250 1255 1260

Asn Ser Ser Phe Arg Gly Tyr Val Gly Lys Thr Gln Ser Val Phe
1265 1270 1275

Lys Phe Asn Ala Lys Asn Ala Ile Ser Phe Thr Asn Ser Thr Asn
1280 1285 1290

Leu Ser Ser Gly Leu Tyr Gln Met Gln Ala Lys Ser Val Leu Phe
1295 1300 1305

Asp Asn Ser Asn Leu Ser Val Ser Val Gly Thr Ser Ser Ile Lys
1310 1315 1320

Ala Asn Ala Ile Asn Leu Ser Gln Asn Ala Ser Ile Asn Ala Ser
1325 1330 1335

Asn His Ser Thr Leu Glu Leu Gln Gly Asp Leu Asn Val Asn Asp
1340 1345 1350

Thr Ser Ser Leu Asn Leu Asn Gln Ser Thr Ile Asn Val Ser Asn
1355 1360 1365

Asn Ala Thr Ile Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly
1370 1375 1380

Ser His Leu Asn Phe Asn Gly Ala Val Asn Phe Asn Ser Ala Asn
1385 1390 1395

Ile Thr Thr Ser Leu Asn Asn Ser Ser Ile Val Phe Lys Gly Ala
1400 1405 1410

Val Ser Leu Gly Gly Gln Phe Asn Leu Ser Asn Asn Ser Ser Leu
1415 1420 1425

Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr Ala Phe Asn
1430 1435 1440

Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe His Gln
1445 1450 1455

Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu Gly Gly Asn Leu Leu
1460 1465 1470

Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys Asn Ser Gln Leu
1475 1480 1485

Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu
1490 1495 1500

Leu Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn Ile Ile
1505 1510 1515

Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe Phe
1520 1525 1530

Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala Lys Asn Gln Thr
1535 1540 1545

Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys Ile Thr Glu
1550 1555 1560

Ser Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln Ile Pro
1565 1570 1575

Gly Ile Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe Asn
1580 1585 1590

Tyr Gln Lys Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser
1595 1600 1605

Asp Asp Ala Gln Gly Val Phe Tyr Leu Thr Ser Asn Val Lys Gly
1610 1615 1620

Tyr Tyr Asn Pro Asn Gln Ser Tyr Gln Ala Ser Gly Ser Asn Asn
1625 1630 1635

Thr Thr Lys Asn Asn Asn Leu Thr Ser Glu Ser Ser Ile Ile Ser
1640 1645 1650

Gln Thr Tyr Asn Ala Gln Gly Asn Pro Ile Ser Ala Leu His Ile
1655 1660 1665

Tyr Asn Lys Gly Tyr Asn Phe Asn Asn Ile Lys Ala Leu Gly Gln
1670 1675 1680

Met Ala Leu Lys Leu Tyr Pro Glu Ile Lys Lys Val Leu Gly Asn
1685 1690 1695

Asp Phe Ser Pro Ser Ser Leu Asn Ala Leu Asn Ser Asn Ala Leu
1700 1705 1710

Asn Gln Leu Thr Lys Leu Ile Thr Pro Asn Asp Trp Lys Asn Ile
1715 1720 1725

Asn Glu Leu Ile Asp Asn Ala Asn Asn Ser Val Val Gln Asn Phe
1730 1735 1740

Asn Asn Gly Thr Leu Ile Val Gly Ala Thr Gln Ile Gly Gln Thr
1745 1750 1755

Asp Thr Asn Ser Ala Val Val Phe Gly Gly Leu Gly Tyr Gln Thr
1760 1765 1770

Pro Cys Asp Tyr Thr Asp Ile Val Cys Gln Lys Phe Arg Gly Thr
1775 1780 1785

Tyr Leu Gly Gln Leu Leu Glu Ser Ser Ser Ala Asp Leu Gly Tyr
1790 1795 1800

Ile Asp Thr Thr Phe Asn Ala Lys Glu Ile Tyr Leu Thr Gly Thr
1805 1810 1815

Leu Gly Ser Gly Asn Ala Trp Gly Thr Gly Gly Ser Ala Ser Val
1820 1825 1830

Thr Phe Asn Ser Gln Thr Ser Leu Ile Leu Asn Gln Ala Asn Ile
1835 1840 1845

Val Ser Ser Gln Thr Asp Gly Ile Phe Ser Met Leu Gly Gln Glu
1850 1855 1860

Gly Ile Asn Lys Val Phe Asn Gln Ala Gly Leu Ala Asn Ile Leu
1865 1870 1875

Gly Glu Val Ala Val Gln Ser Ile Asn Lys Ala Gly Gly Leu Gly
1880 1885 1890

Asn Leu Ile Val Asn Thr Leu Gly Ser Asn Ser Val Ile Gly Gly
1895 1900 1905

Tyr Leu Thr Pro Glu Gln Lys Asn Gln Thr Leu Ser Gln Leu Leu
1910 1915 1920

Gly Gln Asn Asn Phe Asp Asn Leu Met Asn Asp Ser Gly Leu Asn
1925 1930 1935

Thr Ala Ile Lys Asp Leu Ile Arg Gln Lys Leu Gly Phe Trp Thr
1940 1945 1950

Gly Leu Val Gly Gly Leu Ala Gly Leu Gly Gly Ile Asp Leu Gln
1955 1960 1965

Asn Pro Glu Lys Leu Ile Gly Ser Met Ser Ile Asn Asp Leu Leu
1970 1975 1980

Ser Lys Lys Gly Leu Phe Asn Gln Ile Thr Gly Phe Ile Ser Ala
1985 1990 1995

Asn Asp Ile Gly Gln Val Ile Ser Val Met Leu Gln Asp Ile Val
2000 2005 2010

Lys Pro Ser Asn Ala Leu Lys Asn Asp Val Ala Ala Leu Gly Lys
2015 2020 2025

Gln Met Ile Gly Glu Phe Leu Gly Gln Asp Thr Leu Asn Ser Leu
2030 2035 2040

Glu Ser Leu Leu Gln Asn Gln Gln Ile Lys Ser Val Leu Asp Lys
2045 2050 2055

Val Leu Ala Ala Lys Gly Leu Gly Pro Ile Tyr Glu Gln Gly Leu
2060 2065 2070

Gly Asp Leu Ile Pro Asn Leu Gly Lys Lys Gly Leu Phe Ala Pro
2075 2080 2085

Tyr Gly Leu Ser Gln Val Trp Gln Lys Gly Asp Phe Ser Phe Asn
2090 2095 2100

Ala Gln Gly Asn Val Phe Val Gln Asn Ser Thr Phe Ser Asn Ala
2105 2110 2115

Asn Gly Gly Thr Leu Ser Phe Asn Ala Gly Asn Ser Leu Ile Phe
2120 2125 2130

Ala Gly Asn Asn His Ile Ala Phe Thr Asn His Ala Gly Thr Leu
2135 2140 2145

Gln Leu Leu Ser Asp Gln Val Ser Asn Ile Asn Ile Thr Thr Leu
2150 2155 2160

Asn Ala Ser Asn Gly Leu Lys Ile Asn Ala Ala Asn Asn Asn Val
2165 2170 2175

Ser Val Ser Gln Gly Asn Leu Phe Val Ser Ala Ser Cys Ala Gln
2180 2185 2190

Gln Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn Pro Cys Ala Leu
2195 2200 2205

Ser Ala Gln Ser Thr Asn Gly Ala Ser Ser Asn Asn Ala Ser Asn
2210 2215 2220

Asn Ala Pro Ile Ala Leu Ser Asn Asn Asp Glu Ser Leu Met Val
2225 2230 2235

Ala Ala Asn Asp Phe Asn Phe Ser Gly Asn Ile Tyr Ala Asn Gly
2240 2245 2250

Val Val Asp Phe Ser Lys Ile Lys Gly Ser Ala Asn Ile Lys Asn
2255 2260 2265

Leu Tyr Leu Tyr Asn Asn Ala Gln Phe Gln Ala Asn Asn Leu Thr
2270 2275 2280

Ile Ser Asn Gln Ala Val Leu Glu Lys Asn Ala Ser Phe Val Thr
2285 2290 2295

Asn Asn Leu Asn Ile Gln Gly Ala Phe Asn Asn Asn Ala Thr Gln
2300 2305 2310

Lys Ile Glu Val Leu Gln Asn Leu Val Ile Ala Ser Asn Ala Ser
2315 2320 2325

Leu Ser Thr Gly Ile Tyr Gly Leu Glu Val Gly Gly Ala Leu Asn
2330 2335 2340

Asn Ser Gly Ala Ile His Phe Asn Leu Glu Asn Thr Gln Thr Pro
2345 2350 2355

Thr Pro Leu Ile Gln Ala Glu Gly Ile Ile Asn Leu Asn Thr Thr
2360 2365 2370

Gln Thr Pro Phe Met Asn Val Asn Asn Ser Met Ala Asn Asn Thr
2375 2380 2385

Thr Tyr Thr Leu Leu Lys Ser Ser Arg Tyr Ile Asp Tyr Asn Ile
2390 2395 2400

Asn Pro Asn Ser Leu Gln Ser Tyr Leu Asn Leu Tyr Thr Leu Ile
2405 2410 2415

Asn Ile Asn Gly Asn His Ile Glu Glu Lys Asn Gly Ala Leu Thr
2420 2425 2430

Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys Gly Leu Leu Leu
2435 2440 2445

Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln Asn Asn Ile
2450 2455 2460

Leu Ser Leu Ser Val Leu Tyr Asn Gln Val Lys Met Ser Cys Gly
2465 2470 2475

Asp Lys Ala Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr Ile
2480 2485 2490

Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val
2495 2500 2505

Gly Gly Asn Ala Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr
2510 2515 2520

Lys Glu Asn Pro Phe Phe Ala Pro Ile Tyr Leu Lys Asn His Ser
2525 2530 2535

Leu Asn Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr Ala
2540 2545 2550

Ser Leu Ile Ser Asn Pro Asn Phe Arg Asp Asn Ala Thr Asn Leu
2555 2560 2565

Leu Glu Leu Ala Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys
2570 2575 2580

Leu Ser Asp Phe Arg Ser Arg Glu Gly Glu Ser Asp Phe Ser Leu
2585 2590 2595

Leu Glu Leu Lys Asn Lys Arg Phe Ser Asp Pro Asn Pro Glu Val
2600 2605 2610

Phe Val Lys Tyr Ser Gln Leu Ser Lys His Pro Asn Asn Leu Trp
2615 2620 2625

Val Gln Gly Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly
2630 2635 2640

Thr Leu Tyr Gly Leu Asn Ala Gly Tyr Asp Arg Leu Val Lys Asn
2645 2650 2655

Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly Tyr Ser Asp Phe Asn
2660 2665 2670

Gly Asn Ile Met His Ser Leu Gly Asn Asn Val Asp Val Gly Met
2675 2680 2685

Tyr Ala Arg Ala Phe Leu Lys Arg Asn Glu Phe Thr Leu Ser Ala
2690 2695 2700

Asn Glu Thr Tyr Gly Gly Asn Ala Thr Ser Ile Asn Ser Ser Asn
2705 2710 2715

Ser Leu Leu Ser Val Leu Asn Gln Arg Tyr Asn Tyr Asn Thr Trp
2720 2725 2730

Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr Asp Phe Met Phe Lys
2735 2740 2745

Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly Leu Ser Tyr His
2750 2755 2760

Phe Ile Gly Leu Ser Gly Met Lys Gly Asn Asp Ala Ala Tyr Lys
2765 2770 2775

Gln Phe Leu Met His Ser Asn Pro Ser Asn Glu Ser Val Leu Thr
2780 2785 2790

Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr Phe Gly Lys Asn Ser
2795 2800 2805

Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp Leu Leu Ile Lys
2810 2815 2820

Ser Lys Gly Ser Asn Thr Val Arg Phe Val Gly Glu Asn Thr Leu
2825 2830 2835

Leu Tyr Arg Lys Gly Glu Val Phe Asn Thr Phe Ala Ser Val Ile
2840 2845 2850

Thr Gly Gly Glu Met His Leu Trp Arg Leu Val Tyr Val Asn Ala
2855 2860 2865

Gly Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Ile Asn Ile
2870 2875 2880

Thr Gly Asn Val Gly Met Arg Val Ala Phe
2885 2890

<210> 210

<211> 290

<212> PRT

<213> Helicobacter pylori

<400> 210

Met Phe Glu Lys Ile Thr Leu Ala His Lys Asp Leu Phe Ser Arg Phe
1   5   10   15

Leu Ser Ala Gln Lys Ile Val Leu Ser Asp Val Ser Phe Thr Asn Cys
            20   25   30

Phe Leu Trp Gln His Ala Arg Leu Ile Gln Val Ala Val Ile Arg Asp
        35   40   45

Cys Leu Val Ile Gln Thr Thr Tyr Glu Asn Gln Lys Pro Phe Tyr Phe
    50   55   60

Tyr Pro Ile Gly Lys Asn Ala Phe Glu Cys Val Lys Glu Leu Leu Lys
65   70   75   80

Leu Glu Lys Asn Leu Arg Phe His Ser Leu Thr Leu Glu Gln Lys Asp
                85   90   95

Asp Leu Lys Asp Asn Phe Val Gly Val Phe Asp Phe Thr Tyr Asn Arg
            100   105   110

Asp Arg Ser Asp Tyr Val Tyr Ser Ile Glu Glu Leu Ile Ala Leu Lys
        115   120   125

Gly Lys Lys Tyr His Lys Lys Lys Asn His Leu Asn Gln Phe Leu Thr
    130   135   140

Asn His Ala Asn Phe Val Tyr Glu Lys Ile Ser Pro Gln Asn Lys Lys
145   150   155   160

Glu Val Leu Glu Ala Ser Gln Ala Trp Phe Leu Glu Ser Gln Thr Asp
                165   170   175

Asp Ile Gly Leu Ile Asn Glu Asn Lys Gly Ile Gln Ser Val Leu Glu
            180   185   190

Asn Tyr Glu Ser Leu Asp Val Lys Gly Gly Leu Ile Arg Val Asn Gly
        195   200   205

Glu Ile Ala Ser Phe Ser Phe Gly Glu Val Leu Asn Glu Glu Ser Ala
    210   215   220

Leu Ile His Ile Glu Lys Ala Arg Thr Asp Ile Ala Gly Ala Tyr Gln
225   230   235   240

Ile Ile Asn Gln Gln Leu Leu Leu Asn Glu Phe Ser His Leu Thr Tyr
                245   250   255

Ala Asn Arg Glu Glu Asp Leu Gly Leu Glu Gly Leu Arg Arg Ser Lys
260 265 270

Met Ser Tyr Asn Pro Val Phe Leu Ile Asp Lys Tyr Glu Ala Val Ala
275 280 285

Lys Asn
290

<210> 211

<211> 828

<212> PRT

<213> Helicobacter pylori

<400> 211

Met Arg Val Thr Phe Gly Ser Lys Tyr Asn Gln Met Asn Asn Tyr Gln
1 5 10 15

Asn Ala Leu Gln Asn Lys Ile Asn Asp Ala Asn Thr Gln Ile Ala Ser
20 25 30

Gly Leu Lys Ile Arg Tyr Gly Tyr Gln Asn Ser Asp Ile Asn Asn Gln
35 40 45

Asn Leu Lys Phe Gln Tyr Glu Glu Asn Thr Leu Asp Gln Gly Ile Asp
50 55 60

Val Ala Gln Asn Ala Tyr Thr Ser Thr Leu Asn Thr Asp Lys Ala Leu
65 70 75 80

Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu Ile Gln
85 90 95

Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile Ala Asn
100 105 110

Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn Thr Ser
115 120 125

Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg Pro Pro
130 135 140

Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu Asn Val
145 150 155 160

Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly Gln Asp
165 170 175

Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr Thr Asn
180 185 190

Ile Lys Leu Phe Asn Gln Asn Lys Leu His Pro Asp Val Met Asp Ala
195 200 205

Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro Ser Asp
210 215 220

Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asp Pro Thr Asn Asp
225 230 235 240

Pro Lys Glu Phe Phe Tyr Leu Gln Gly Val Arg Pro Asp Gly Ser Ser
245 250 255

Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln Glu Ser
260 265 270

Ala Ser Lys Val Ser Asp Leu Leu Asp Lys Ile Ala His Ala Tyr Gly
275 280 285

Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn Trp Gly
290 295 300

Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu Asp Phe
305 310 315 320

His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala Leu Arg
325 330 335

Ser Ser Gly Lys Arg Val Thr Glu Tyr Ile Lys Ser Ala Phe Val Thr
340 345 350

Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr Asn Pro
355 360 365

Lys Val Leu Glu Val Pro Ser Val Phe Val Thr Lys Asp Asn Val Leu
370 375 380

Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Ser Val Glu
385 390 395 400

Thr Leu Lys Ile Asn Ala Ser Arg Leu Asp Glu Thr Ser Ala Ile Lys
405 410 415

Ile Pro Asn Leu Pro Val Tyr Leu Asp Ile Pro Ile Leu Leu Asp Val
420 425 430

Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Lys Arg Phe
435 440 445

Asn Asn Glu Val Asp Val Glu Ile Glu Thr Asn Gly Arg Leu Arg Ile
    450   455   460

Ile Asp Asn Ser Ser Lys Glu Ser Pro Ile Ser Leu Ala Leu Ser Ala
465   470   475   480

Leu Asp Ala Lys Gly Leu Glu Val Ala Gly Ile Pro Thr Asn Asn Ala
                485   490   495

Ser Glu Tyr Gln Lys Thr Tyr Phe Asn Lys Glu Gly Ala Lys Leu Glu
            500   505   510

Ser Asn Val Ala Gln Thr Ala Gln Asn Gly Ala Ala Asn Gly Ser Thr
        515   520   525

Lys Leu Ser Glu Ala Ala Lys Gly Ser Leu Glu Asn Ser Val Phe Asn
    530   535   540

Met Lys Leu Asn Asp Val Asn Gly Leu Phe Leu Glu Ala Gln Met Asn
545   550   555   560

Leu Asp Asn Asn Gly Ala Phe Leu Ser Leu Pro Asn Gly Ile Lys Ile
                565   570   575

Pro Leu Tyr Asp Pro Thr Ser Ala Asp Ile Gln Ala Ser Lys Pro Asn
            580   585   590

Glu Val Thr Tyr Arg Gln Leu Met Asp Ala Met Ser Ile Ala Leu Asn
        595   600   605

Tyr Ser Asn Thr Asp Pro Ala Ile Tyr Gln Gln Ile Ser Asp Asn Pro
    610   615   620

Thr Ser Lys Glu Ser Lys Glu Arg Phe Ile Gly Leu Leu Lys Gln Ala
625   630   635   640

Lys Asp Asn Leu Ser Val Asn Leu Asn Glu Glu Gly Lys Val Ile Ile
                645   650   655

Gln Asp Asn Met His Ser Asn Thr Lys Met Gln Phe Met Leu Phe Asp
            660   665   670

Lys Asp Ala Asn Asp Phe Ser Gln Asn Ala Leu His Ser Asp Lys Pro
        675   680   685

Ser Leu Lys Leu Asn Ala Asn Asn Ala Leu Ile Ile Asp Lys Pro Ser
    690   695   700

Val Asn Phe Phe Asp Gln Leu Glu Asn Thr Ile Thr Ser Val Arg Lys
705   710   715   720

Gly Ile Tyr Arg Pro Asp Ala Leu Gly Asp Thr Tyr Ser Ser Asp Met
                725   730   735

Arg Asn Leu Gly Ile Gln Asn Gly Ile Thr Leu Ile Asp His Leu Ser
            740   745   750

Asp His Ile Glu Lys Met Ile Ala Lys Asn Gly Ala His Gly Lys Ala
        755   760   765

Phe Glu Asn Ile Ile Arg Arg Asn Glu Val Leu Lys Thr Gln Val Gln
    770   775   780

Ser Ile Arg Gly Glu Thr Thr Gly Thr Asp Met Ala Glu Thr Tyr Asn
785   790   795   800

Lys Phe Ser Asn Leu Thr Asn Asn Tyr Asn Ala Val Leu Ala Ser Thr
                805   810   815

Asn Lys Ile Asn Asn Leu Ser Leu Thr Lys Tyr Leu
            820   825

<210> 212

<211> 538

<212> PRT

<213> Helicobacter pylori

<400> 212

Met Asp Arg Ala Lys Phe Ile Phe Val Thr Gly Gly Val Leu Ser Ser
1   5   10   15

Leu Gly Lys Gly Ile Ser Ser Ser Ser Ile Ala Thr Leu Leu Gln His
            20   25   30

Cys Asn Tyr Gln Val Ser Ile Leu Lys Ile Asp Pro Tyr Ile Asn Ile
        35   40   45

Asp Pro Gly Thr Met Ser Pro Leu Glu His Gly Glu Val Phe Val Thr
    50   55   60

Ser Asp Gly Ala Glu Thr Asp Leu Asp Ile Gly His Tyr Glu Arg Phe
65   70   75   80

Leu Asn Arg Asn Leu Thr Arg Leu Asn Asn Phe Thr Thr Gly Gln Ile
                85   90   95

Phe Ser Ser Val Ile Glu Asn Glu Arg Lys Gly Glu Tyr Leu Gly Lys
            100   105   110

Thr Ile Gln Ile Val Pro His Val Thr Asp Glu Ile Lys Arg Arg Ile
115 120 125

Lys Ser Ala Ala Lys Gly Leu Asp Phe Leu Ile Val Glu Val Gly Gly
130 135 140

Thr Val Gly Asp Met Glu Gly Met Phe Tyr Leu Glu Ala Ile Arg Gln
145 150 155 160

Leu Lys Leu Glu Leu Gly Asn Glu Lys Val Ile Asn Val His Val Thr
165 170 175

Leu Ile Pro Tyr Ile Gln Thr Thr Asn Glu Leu Lys Thr Lys Pro Thr
180 185 190

Gln His Ser Val Gln Glu Leu Arg Arg Leu Gly Val Thr Pro Gln Ile
195 200 205

Ile Leu Ala Arg Ser Pro Lys Pro Leu Asp Lys Glu Leu Lys Asn Lys
210 215 220

Ile Ala Leu Ser Cys Asp Val Glu Gln Asp Ser Val Ile Val Ala Thr
225 230 235 240

Asp Thr Lys Ser Ile Tyr Ala Cys Pro Ile Leu Phe Leu Gln Glu Gly
245 250 255

Ile Leu Thr Pro Ile Ala Arg Arg Phe Asn Leu Asn Lys Leu His Pro
260 265 270

Lys Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro Lys
275 280 285

His Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys Glu
290 295 300

Ser Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His Leu
305 310 315 320

Asp Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn Glu
325 330 335

Lys Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly Phe
340 345 350

Gly Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala Arg
355 360 365

Leu Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu Ala
370 375 380

Ile Val Glu Phe Cys Arg Asn Val Leu Gly Leu Lys Gly Ala Asn Ser
385 390 395 400

Thr Glu Phe Asn Gln Arg Cys Glu Tyr Pro Val Val Tyr Leu Ile Gly
405 410 415

Asp Phe Met Asp Gln Asn His Gln Lys Gln Val Arg Thr Tyr Asn Ser
420 425 430

Pro Leu Gly Gly Thr Met Arg Leu Gly Glu Tyr Glu Cys Glu Ile Met
435 440 445

Pro Asn Ser Leu Leu Glu Lys Ala Tyr Lys Lys Pro Ser Ile Lys Glu
450 455 460

Arg His Arg His Arg Tyr Glu Ile Asn Pro Lys Tyr Arg Gln Glu Trp
465 470 475 480

Glu Asn Lys Gly Leu Lys Val Val Gly Phe Gly Ser Asn His Leu Ile
485 490 495

Glu Ala Ile Glu Leu Glu Asp His Pro Phe Phe Val Gly Val Gln Phe
500 505 510

His Pro Glu Phe Thr Ser Arg Leu Gln Ser Pro Asn Pro Ile Ile Leu
515 520 525

Asp Phe Ile Lys Ser Ala Leu Ser Lys Ser
530 535

<210> 213

<211> 567

<212> PRT

<213> Helicobacter pylori

<400> 213

Leu Asp Leu Lys Val Leu Leu Gln Arg Ile Val Asp Phe Phe Ile Lys
1 5 10 15

Leu Asn Lys Lys Gln Lys Ile Ala Leu Ile Ala Ala Gly Val Leu Ile
20 25 30

Thr Ala Leu Leu Val Phe Leu Leu Leu Tyr Pro Phe Lys Glu Lys Asp
35 40 45

Tyr Thr Gln Gly Gly Tyr Gly Val Leu Phe Glu Gly Leu Asp Ser Ser
50 55 60

Asp Asn Ala Leu Ile Leu Gln His Leu Gln Gln Asn Gln Ile Pro Tyr
65 70 75 80

Lys Val Ser Lys Asp Asp Thr Ile Leu Ile Pro Lys Asp Lys Val Tyr
85 90 95

Glu Glu Arg Ile Thr Leu Ala Ser Gln Gly Ile Pro Lys Thr Ser Lys
100 105 110

Val Gly Phe Glu Ile Phe Asp Thr Lys Asp Phe Gly Ala Thr Asp Phe
115 120 125

Asp Gln Asn Ile Lys Leu Ile Arg Ala Ile Glu Gly Glu Leu Ser Arg
130 135 140

Thr Ile Glu Ser Leu Asn Pro Ile Leu Lys Ala Asn Val His Ile Ala
145 150 155 160

Ile Pro Lys Asp Ser Val Phe Val Ala Lys Glu Val Pro Pro Ser Ala
165 170 175

Ser Val Met Leu Lys Leu Lys Pro Asp Met Lys Leu Ser Pro Thr Gln
180 185 190

Ile Leu Gly Ile Lys Asn Leu Ile Ala Ala Ala Val Pro Lys Leu Thr
195 200 205

Ile Glu Asn Val Lys Ile Val Asn Glu Asn Gly Glu Ser Ile Gly Glu
210 215 220

Gly Asp Ile Leu Glu Asn Ser Lys Glu Leu Ala Leu Glu Gln Leu His
225 230 235 240

Tyr Lys Gln Asn Phe Glu Asn Ile Leu Glu Asn Lys Ile Val Asn Ile
245 250 255

Leu Ala Pro Ile Val Gly Gly Lys Asn Lys Val Val Ala Arg Val Asn
260 265 270

Ala Glu Phe Asp Phe Ser Gln Lys Lys Ser Thr Lys Glu Thr Phe Asp
275 280 285

Pro Asn Asn Val Val Arg Ser Glu Gln Asn Leu Glu Glu Lys Lys Glu
290 295 300

Gly Ala Ser Lys Lys Gln Val Gly Gly Val Pro Gly Val Val Ser Asn
305 310 315 320

Ile Gly Pro Val Gln Gly Leu Lys Asp Asn Lys Glu Pro Glu Lys Tyr
325 330 335

Glu Lys Ser Gln Asn Thr Thr Asn Tyr Glu Val Gly Lys Thr Ile Ser
340 345 350

Glu Ile Lys Gly Glu Phe Gly Thr Leu Val Arg Leu Asn Ala Ala Val
355 360 365

Val Val Asp Gly Lys Tyr Lys Ile Ala Leu Lys Asp Gly Val Asn Thr
370 375 380

Leu Glu Tyr Glu Pro Leu Ser Asp Glu Ser Leu Gln Lys Ile Asn Ala
385 390 395 400

Leu Val Lys Gln Ala Ile Gly Tyr Asn Gln Asn Arg Gly Asp Asp Val
405 410 415

Ala Val Ser Asn Phe Glu Phe Asn Pro Met Ala Pro Val Ile Asp Asn
420 425 430

Ala Thr Leu Ser Glu Lys Ile Met His Lys Thr Gln Lys Ile Leu Gly
435 440 445

Ser Phe Thr Pro Leu Ile Lys Tyr Ile Leu Val Phe Ile Val Leu Phe
450 455 460

Ile Phe Tyr Lys Lys Val Ile Val Pro Phe Ser Glu Arg Met Leu Glu
465 470 475 480

Val Val Pro Asp Glu Asp Lys Glu Val Lys Ser Met Phe Glu Glu Met
485 490 495

Asp Glu Glu Glu Asp Glu Leu Asn Lys Leu Gly Asp Leu Arg Lys Lys
500 505 510

Val Glu Asp Gln Leu Gly Leu Asn Ala Ser Phe Ser Glu Glu Glu Val
515 520 525

Arg Tyr Glu Ile Ile Leu Glu Lys Ile Arg Gly Thr Leu Lys Glu Arg
530 535 540

Pro Asp Glu Ile Ala Met Leu Phe Lys Leu Leu Ile Lys Asp Glu Ile
545 550 555 560

Ser Ser Asp Gly Ala Lys Gly
565

<210> 214

<211> 448

<212> PRT

<213> Helicobacter pylori

<400> 214

Met Tyr Val Glu Lys Ile Leu Gln Ser Leu Gln Lys Lys Tyr Pro Tyr
1   5   10   15

Gln Lys Glu Phe His Gln Ala Val Tyr Glu Ala Ile Thr Ser Leu Lys
            20   25   30

Pro Leu Leu Asp Ser Asp Lys Ser Tyr Glu Lys His Ala Ile Leu Glu
        35   40   45

Arg Leu Ile Glu Pro Glu Arg Glu Ile Phe Phe Arg Val Cys Trp Leu
    50   55   60

Asp Asp Asn Asn Gln Ile Gln Val Asn Arg Gly Cys Arg Val Glu Phe
65   70   75   80

Asn Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser
                85   90   95

Val Asn Glu Ser Val Ile Lys Phe Leu Gly Phe Glu Gln Val Leu Lys
            100   105   110

Asn Ser Leu Thr Thr Leu Ala Met Gly Gly Ala Lys Gly Gly Ser Asp
        115   120   125

Phe Asp Pro Lys Gly Lys Ser Glu His Glu Ile Met Arg Phe Cys Gln
    130   135   140

Ala Phe Met Asn Glu Leu Tyr Arg His Ile Gly Ala Thr Thr Asp Val
145   150   155   160

Pro Ala Gly Asp Ile Gly Val Gly Glu Arg Glu Ile Gly Tyr Leu Phe
                165   170   175

Gly Gln Tyr Lys Lys Leu Val Asn Arg Phe Glu Gly Val Leu Thr Gly
            180   185   190

Lys Gly Leu Thr Tyr Gly Gly Ser Leu Cys Arg Lys Glu Ala Thr Gly
        195   200   205

Tyr Gly Cys Val Tyr Phe Ala Glu Glu Met Leu Gln Glu Arg Asn Ser
    210   215   220

Ser Leu Glu Gly Lys Val Cys Ser Val Ser Gly Ser Gly Asn Val Ala
225   230   235   240

Ile Tyr Thr Ile Glu Lys Leu Leu Gln Ile Gly Ala Lys Pro Val Thr
                245   250   255

Ala Ser Asp Ser Asn Gly Met Ile Tyr Asp Lys Asp Gly Ile Asp Leu
260 265 270

Glu Leu Leu Lys Glu Ile Lys Glu Val Arg Arg Gly Arg Ile Lys Glu
275 280 285

Tyr Ala Leu Glu Lys Lys Ser Ala Glu Tyr Thr Pro Thr Glu Asn Tyr
290 295 300

Pro Lys Gly Gly Asn Ala Val Trp His Val Pro Cys Phe Ala Ala Phe
305 310 315 320

Pro Ser Ala Thr Glu Asn Glu Leu Ser Val Leu Asp Ala Lys Thr Leu
325 330 335

Leu Ser Asn Gly Cys Lys Cys Val Ala Glu Gly Ala Asn Met Pro Ser
340 345 350

Ser Asn Glu Ala Ile Gly Leu Phe Leu Gln Ala Lys Ile Ser Tyr Gly
355 360 365

Ile Gly Lys Ala Ala Asn Ala Gly Gly Val Ser Val Ser Gly Leu Glu
370 375 380

Met Ala Gln Asn Ala Ser Met His Pro Trp Ser Phe Glu Val Val Asp
385 390 395 400

Ala Lys Leu His His Ile Met Lys Glu Ile Tyr Lys Asn Val Ser Gln
405 410 415

Thr Ala Lys Glu Phe Lys Asp Pro Thr Asn Phe Val Leu Gly Ala Asn
420 425 430

Ile Ala Gly Phe Arg Lys Val Ala Ser Ala Met Ile Ala Gln Gly Val
435 440 445

<210> 215

<211> 803

<212> PRT

<213> Helicobacter pylori

<400> 215

Met Asp Asp Leu Gln Glu Ile Met Glu Asp Phe Leu Ile Glu Ala Phe
1 5 10 15

Glu Met Asn Glu Gln Leu Asp Gln Asp Leu Val Glu Leu Glu His Asn
20 25 30

Pro Glu Asp Leu Asp Leu Leu Asn Arg Ile Phe Arg Val Ala His Thr
35 40 45

Ile Lys Gly Ser Ser Ser Phe Leu Asn Leu Asn Ile Leu Thr His Leu
50 55 60

Thr His Asn Met Glu Asp Val Leu Asn Arg Ala Arg Lys Gly Glu Ile
65 70 75 80

Lys Ile Thr Pro Asp Ile Met Asp Val Val Leu Arg Ser Ile Asp Leu
85 90 95

Met Lys Thr Leu Leu Val Thr Ile Arg Asp Thr Gly Ser Asp Thr Asn
100 105 110

Asn Gly Lys Glu Asn Glu Ile Glu Glu Ala Val Lys Gln Leu Gln Ala
115 120 125

Ile Thr Ser Gln Asn Leu Glu Ser Ala Lys Glu Arg Thr Thr Glu Ala
130 135 140

Pro Gln Lys Glu Asn Lys Glu Glu Thr Lys Glu Glu Ala Lys Glu Glu
145 150 155 160

Asn Lys Glu Asn Lys Ala Lys Ala Pro Thr Ala Glu Asn Thr Ser Ser
165 170 175

Asp Asn Pro Leu Ala Asp Glu Pro Asp Leu Asp Tyr Ala Asn Met Ser
180 185 190

Ala Glu Glu Val Glu Ala Glu Ile Glu Arg Leu Leu Asn Lys Arg Gln
195 200 205

Glu Ala Asp Lys Glu Arg Arg Ala Gln Lys Lys Gln Glu Ala Lys Pro
210 215 220

Lys Gln Glu Val Thr Pro Thr Lys Glu Thr Pro Lys Ala Pro Lys Thr
225 230 235 240

Glu Thr Lys Ala Lys Ala Lys Ala Asp Thr Glu Glu Asn Lys Ala Pro
245 250 255

Ser Ile Gly Val Glu Gln Thr Val Arg Val Asp Val Arg Arg Leu Asp
260 265 270

His Leu Met Asn Leu Ile Gly Glu Leu Val Leu Gly Lys Asn Arg Leu
275 280 285

Ile Arg Ile Tyr Ser Asp Val Glu Glu Arg Tyr Asp Gly Glu Lys Phe
290 295 300

Leu Glu Glu Leu Asn Gln Val Val Ser Ser Ile Ser Ala Val Thr Thr
305 310 315 320

Asp Leu Gln Leu Ala Val Met Lys Thr Arg Met Gln Pro Val Gly Lys
325 330 335

Val Phe Asn Lys Phe Pro Arg Met Val Arg Asp Leu Ser Arg Glu Leu
340 345 350

Gly Lys Ser Ile Glu Leu Ile Ile Glu Gly Glu Glu Thr Glu Leu Asp
355 360 365

Lys Ser Ile Val Glu Glu Ile Gly Asp Pro Leu Ile His Ile Ile Arg
370 375 380

Asn Ser Cys Asp His Gly Ile Glu Pro Leu Glu Glu Arg Arg Lys Leu
385 390 395 400

Asn Lys Pro Glu Thr Gly Lys Val Gln Leu Ser Ala Tyr Asn Glu Gly
405 410 415

Asn His Ile Val Ile Lys Ile Ser Asp Asp Gly Lys Gly Leu Asp Pro
420 425 430

Val Met Leu Lys Glu Lys Ala Ile Glu Lys Gly Val Ile Ser Glu Arg
435 440 445

Asp Ala Glu Gly Met Ser Asp Arg Glu Ala Phe Asn Leu Ile Phe Lys
450 455 460

Pro Gly Phe Ser Thr Ala Lys Val Val Ser Asn Val Ser Gly Arg Gly
465 470 475 480

Val Gly Met Asp Val Val Lys Thr Asn Ile Glu Lys Leu Asn Gly Ile
485 490 495

Ile Glu Ile Asp Ser Glu Val Gly Val Gly Thr Thr Gln Lys Leu Lys
500 505 510

Ile Pro Leu Thr Leu Ala Ile Ile Gln Ala Leu Leu Val Gly Val Gln
515 520 525

Glu Glu Tyr Tyr Ala Ile Pro Leu Ser Ser Val Leu Glu Thr Val Arg
530 535 540

Ile Ser Gln Asp Glu Ile Tyr Thr Val Asp Gly Lys Ser Val Leu Arg
545 550 555 560

Leu Arg Asp Glu Val Leu Ser Leu Val Arg Leu Ser Asp Ile Phe Lys
565 570 575

Val Asp Ala Ile Leu Glu Ser Asn Ser Asp Val Tyr Val Val Ile Ile
580 585 590

Gly Leu Ala Asp Gln Lys Ile Gly Val Ile Val Asp Tyr Leu Ile Gly
595 600 605

Gln Glu Glu Val Val Ile Lys Ser Leu Gly Tyr Tyr Leu Lys Asn Thr
610 615 620

Arg Gly Ile Ala Gly Ala Thr Val Arg Gly Asp Gly Lys Ile Thr Leu
625 630 635 640

Ile Val Asp Val Gly Ala Met Met Asp Met Ala Lys Ser Ile Lys Val
645 650 655

Asn Ile Thr Thr Leu Met Asn Glu Ser Glu Asn Thr Lys Ser Lys Asn
660 665 670

Ser Pro Ser Asp Tyr Ile Val Leu Ala Ile Asp Asp Ser Ser Thr Asp
675 680 685

Arg Ala Ile Ile Arg Lys Cys Leu Lys Pro Leu Gly Ile Thr Leu Leu
690 695 700

Glu Ala Thr Asn Gly Leu Glu Gly Leu Glu Met Leu Lys Asn Gly Asp
705 710 715 720

Lys Ile Pro Asp Ala Ile Leu Val Asp Ile Glu Met Pro Lys Met Asp
725 730 735

Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys Tyr Asn Lys Phe Lys Asn
740 745 750

Leu Pro Leu Ile Ala Val Thr Ser Arg Val Thr Lys Thr Asp Arg Met
755 760 765

Arg Gly Val Glu Ser Gly Met Thr Glu Tyr Ile Thr Lys Pro Tyr Ser
770 775 780

Gly Glu Tyr Leu Thr Thr Val Val Lys Arg Ser Ile Lys Leu Glu Gly
785 790 795 800

Asp Gln Ser

<210> 216

<211> 429

<212> PRT

<213> Helicobacter pylori

<400> 216

Val Ile Glu Leu Asp Ile Asn Ala Ser Asp Lys Ser Leu Ser His Arg
1   5   10   15

Ala Val Ile Phe Ser Leu Leu Ala Gln Lys Pro Cys Phe Val Arg Asn
            20   25   30

Phe Leu Met Gly Glu Asp Cys Leu Ser Ser Leu Glu Ile Ala Gln Asn
        35   40   45

Leu Gly Ala Lys Val Glu Asn Thr Ala Lys Asn Ser Phe Lys Ile Thr
    50   55   60

Pro Pro Thr Thr Ile Lys Glu Pro Asn Lys Ile Leu Asn Cys Asn Asn
65   70   75   80

Ser Gly Thr Thr Met Arg Leu Tyr Ser Gly Leu Leu Ser Ala Gln Lys
                85   90   95

Gly Leu Phe Val Leu Ser Gly Asp Asn Ser Leu Asn Ala Arg Pro Met
            100   105   110

Lys Arg Ile Ile Glu Pro Leu Lys Ala Phe Gly Ala Lys Ile Leu Gly
        115   120   125

Arg Glu Asp Asn His Phe Ala Pro Leu Val Ile Leu Gly Ser Pro Leu
    130   135   140

Lys Ala Cys His Tyr Glu Ser Pro Ile Ala Ser Ala Gln Val Lys Ser
145   150   155   160

Ala Phe Ile Leu Ser Ala Leu Gln Ala Gln Gly Ala Ser Thr Tyr Lys
                165   170   175

Glu Ser Glu Leu Ser Arg Asn His Thr Glu Ile Met Leu Lys Ser Leu
            180   185   190

Gly Ala Asp Ile His Asn Gln Asp Gly Val Leu Lys Ile Ser Pro Leu
        195   200   205

Glu Lys Pro Leu Glu Ala Phe Asp Phe Thr Ile Ala Asn Asp Pro Ser
    210   215   220

Ser Ala Phe Phe Phe Ala Leu Ala Cys Ala Ile Thr Pro Lys Ser Arg
225   230   235   240

Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg Ile Glu Ala Phe
                245   250   255

Glu Val Leu Lys Lys Met Gly Ala Ser Ile Glu Tyr Ala Ile Gln Ser
            260   265   270

Lys Asp Leu Glu Met Ile Gly Asp Ile Tyr Val Glu His Ala Pro Leu
        275   280   285

Lys Ala Ile Asn Ile Asp Gln Asn Ile Ala Ser Leu Ile Asp Glu Ile
    290   295   300

Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly Lys Ser Met Val
305   310   315   320

Lys Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp Arg Ile Lys Ala
                325   330   335

Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys Glu Glu Phe Glu
            340   345   350

Asp Gly Phe Tyr Val Glu Gly Leu Glu Asp Ile Ser Pro Leu Lys Gln
        355   360   365

Arg Phe Ser Arg Ile Lys Pro Pro Leu Ile Lys Ser Phe Asn Asp His
    370   375   380

Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala Leu Pro Leu Glu
385   390   395   400

Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro Gln Phe Lys His
                405   410   415

Leu Leu Asn Gln Phe Lys Lys Gly Ser Leu Asn Gly Asn
            420   425

<210> 217

<211> 196

<212> PRT

<213> Helicobacter pylori

<400> 217

Leu Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu
1   5   10   15

Gln Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu
            20   25   30

Glu Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg
        35   40   45

Leu Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly
50 55 60

Lys Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser
65 70 75 80

Ser Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser
85 90 95

Met Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr
100 105 110

Ile Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp
115 120 125

Glu Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala
130 135 140

Leu Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp
145 150 155 160

Leu Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met
165 170 175

Lys Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser
180 185 190

Val Asn Lys Lys
195

<210> 218

<211> 508

<212> PRT

<213> Helicobacter pylori

<400> 218

Met Ile Leu Val Leu Asp Phe Gly Ser Gln Tyr Thr Gln Leu Ile Ala
1 5 10 15

Arg Arg Leu Arg Glu Arg Gly Ile Tyr Thr Glu Ile Val Pro Phe Phe
20 25 30

Glu Ser Ile Glu Asn Ile Gln Lys Lys Ala Pro Lys Gly Leu Ile Leu
35 40 45

Ser Gly Gly Pro Ala Ser Val Tyr Ala Lys Asp Ala Tyr Lys Pro Ser
50 55 60

Gly Lys Ile Phe Asp Leu Asn Val Pro Ile Leu Gly Ile Cys Tyr Gly
65 70 75 80

Met Gln Tyr Leu Val Asp Phe Phe Gly Gly Val Val Val Gly Ala Asn
85 90 95

Glu Gln Glu Phe Gly Lys Ala Val Leu Glu Ile Thr Gln Asn Ser Val
100 105 110

Ile Phe Glu Gly Val Lys Ile Lys Ser Leu Val Trp Met Ser His Met
115 120 125

Asp Lys Val Ile Glu Leu Pro Lys Gly Phe Thr Thr Leu Ala Lys Ser
130 135 140

Pro Asn Ser Pro His Cys Ala Ile Glu Asn Gly Lys Ile Phe Gly Leu
145 150 155 160

Gln Phe His Pro Glu Val Val Gln Ser Glu Glu Gly Gly Lys Ile Leu
165 170 175

Glu Asn Phe Ala Leu Leu Val Cys Gly Cys Glu Lys Thr Trp Gly Met
180 185 190

Gln His Phe Ala Gln Arg Glu Ile Ala Arg Leu Lys Glu Lys Ile Ala
195 200 205

Asn Ala Lys Val Leu Cys Ala Val Ser Gly Gly Val Asp Ser Thr Val
210 215 220

Val Ala Thr Leu Leu His Arg Ala Ile Lys Asp Asn Leu Ile Ala Val
225 230 235 240

Phe Val Asp His Gly Leu Leu Arg Lys Asn Glu Lys Glu Arg Val Gln
245 250 255

Ala Met Phe Lys Asp Leu Lys Ile Pro Leu Asn Thr Ile Asp Ala Lys
260 265 270

Glu Val Phe Leu Ser Lys Leu Lys Gly Val Ser Glu Pro Glu Leu Lys
275 280 285

Arg Lys Ile Ile Gly Glu Thr Phe Ile Glu Val Phe Glu Lys Glu Ala
290 295 300

Lys Lys His His Leu Lys Gly Lys Ile Glu Phe Leu Ala Gln Gly Thr
305 310 315 320

Leu Tyr Pro Asp Val Ile Glu Ser Val Ser Val Lys Gly Pro Ser Lys
325 330 335

Val Ile Lys Thr His His Asn Val Gly Gly Leu Pro Glu Trp Met Asp
340 345 350

Phe Lys Leu Ile Glu Pro Leu Arg Glu Leu Phe Lys Asp Glu Val Arg
355 360 365

Leu Leu Gly Lys Glu Leu Gly Val Ser Gln Asp Phe Leu Met Arg His
370 375 380

Pro Phe Pro Gly Pro Gly Leu Ala Val Arg Ile Leu Gly Glu Ile Ser
385 390 395 400

Glu Ser Lys Ile Lys Arg Leu Gln Glu Ala Asp Phe Ile Phe Ile Glu
405 410 415

Glu Leu Lys Lys Ala Asn Leu Tyr Asp Lys Val Trp Gln Ala Phe Cys
420 425 430

Val Leu Leu Asn Val Asn Ser Val Gly Val Met Gly Asp Asn Arg Thr
435 440 445

Tyr Glu Asn Ala Ile Cys Leu Arg Ala Val Asn Ala Ser Asp Gly Met
450 455 460

Thr Ala Ser Phe Ser Phe Leu Glu His Ser Phe Leu Glu Lys Val Ser
465 470 475 480

Asn Arg Ile Thr Asn Glu Val Ser Gly Ile Asn Arg Val Val Tyr Asp
485 490 495

Ile Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu
500 505

<210> 219

<211> 268

<212> PRT

<213> Helicobacter pylori

<400> 219

Met Lys Val Asn Lys Gly Phe Lys Phe Arg Leu Tyr Pro Thr Lys Glu
1 5 10 15

Gln Gln Asp Lys Leu Gln His Cys Phe Phe Val Tyr Asn Gln Ala Tyr
20 25 30

Asn Ile Gly Leu Asn Glu Leu Gln Glu Gln Tyr Glu Thr Asn Lys Asp
35 40 45

Ser Pro Pro Lys Glu Arg Lys Tyr Lys Lys Ser Ser Glu Leu Asp Asn
50 55 60

Ala Ile Lys Gln Cys Leu Arg Ala Arg Asp Leu Pro Phe Ser Ala Val
65 70 75 80

Ile Ala Gln Gln Ala Arg Met Asn Val Glu Arg Ala Leu Lys Asp Ala
85 90 95

Phe Lys Val Lys Asn Arg Gly Phe Pro Lys Phe Lys Asn Ser Lys Ser
100 105 110

Ala Lys Gln Ser Phe Ser Trp Asn Asn Gln Gly Phe Ser Ile Lys Glu
115 120 125

Ser Asp Asp Glu Cys Phe Lys Thr Phe Thr Leu Met Lys Met Pro Leu
130 135 140

Leu Met Arg Met His Arg Arg Leu Pro Pro Asn Phe Lys Val Lys Gln
145 150 155 160

Ile Ser Ile Ser Cys Ser His Arg Lys Tyr Phe Val Ser Phe Ser Val
165 170 175

Glu Tyr Glu Gln Asp Ile Thr Pro Ile Lys Asn Thr Lys Asn Gly Val
180 185 190

Gly Leu Asp Leu Asn Ile Leu Asp Thr Ala Cys Ser Cys Glu Ile Asn
195 200 205

Asn His Asp Lys Leu Thr Asp Phe Lys Gln Tyr Gln Thr Asp Met Lys
210 215 220

Glu Leu Leu Gly Ile Glu Ile Asp Glu Glu Leu Asp Thr Lys Arg Leu
225 230 235 240

Ile Pro Thr Tyr Ser Lys Leu Tyr Ser Leu Lys Lys Tyr Ser Lys Lys
245 250 255

Phe Lys Arg Leu Gln Arg Lys Gln Ser Arg Arg Cys
260 265

<210> 220

<211> 858

<212> PRT

<213> Helicobacter pylori

<400> 220

Met Leu Glu Ser Ala Leu Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu
1   5   10   15

Leu Val Gly Phe Val Pro Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn
            20   25   30

Ile Leu Gly Leu Tyr Asp Asp Ala Phe Ile Ile Thr Lys Gln Glu Asn
        35   40   45

Leu Val Gly Ile Ile Ser Leu Gln Gly Leu Ser Tyr Ser Asn Leu Met
    50   55   60

Gln Lys Asp Leu Glu Gly Tyr Phe Asp Ala Arg Gln Asn Val Leu Asn
65   70   75   80

Thr Ile Ser Lys Asp Ile Gln Leu Arg Ile Val Ala Lys Arg Arg Lys
                85   90   95

Glu Phe Ile Asn Gln Ser Pro Asn Ile Asp Asn Ile Tyr Ala Lys Ala
            100   105   110

Ile Ile Thr Gln Phe Glu Ser Lys Gly Ile Tyr Lys Thr Glu Tyr Phe
        115   120   125

Leu Val Phe Glu Thr Ile Thr Ser Asn Val Lys Ser Phe Phe Glu Lys
    130   135   140

Lys Lys Leu Glu Met Thr Thr Ser Ile Asn Glu Glu Leu Glu Glu Ser
145   150   155   160

Ser Lys Glu Asp Lys Gln Glu Asn Glu Asn Ser Ser Asn Glu Thr His
                165   170   175

Ser Asn Thr Ser Ser Lys Lys Asp Lys Lys Asn Lys Phe Lys Lys Lys
            180   185   190

Ile Thr Phe Ser Thr Lys Ser Lys Arg Ala Leu Leu Ile Gln Thr Ile
        195   200   205

Glu Arg Val Lys Asn Ala Leu Lys Glu Phe Lys Pro Thr Leu Leu Asn
    210   215   220

Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr Ile Asn Gly Lys Tyr
225   230   235   240

Ile Ala Phe Asn Pro Lys Leu Lys Arg Leu Ser Asp Ser Tyr Ile Ala
                245   250   255

Ser Asn Val His Phe Lys Lys Asp Tyr Phe Val Ile Glu Phe Gln Asn
            260   265   270

Gln Asn Thr Phe Cys Ala Cys Val Gly Ile Lys Ala Tyr Glu Ser Glu
275 280 285

Glu Ile Ser Ser Leu Pro Ile Ser Thr Leu Leu His Thr Gln Ile Glu
290 295 300

Leu Asp Leu Ile Phe His Ile Arg Ser Leu Gly Gln Phe Glu Ser Leu
305 310 315 320

Asn Phe Leu Lys Thr Lys Lys Lys Leu Thr Leu Ser Lys Ile Val Lys
325 330 335

Ala Asp Ile Asp Asn Tyr Ile Glu Leu Val Gln Ala Asn Arg Leu Ser
340 345 350

Met Gln Glu Cys Ala Leu Asn Leu Val Ile Arg Ala Lys Ser Lys Ala
355 360 365

Lys Leu Asp Lys Ser Leu Lys Glu Ile Leu Ser Leu Leu Asn Asn Ala
370 375 380

Gly Leu Gly Ser Val Thr Glu Thr Ile Gly Leu Lys Pro Ser Tyr Phe
385 390 395 400

Ser Phe Phe Pro Asn Asn Ala Asn Ile Asn Pro Arg Met Arg His Gln
405 410 415

Thr Ser Gln Val Ile Ala Ser Leu Ile Leu Phe Glu Lys Asn Asn Thr
420 425 430

Gly Phe Arg Ala Asn Ser Trp Gly Asp Met Pro Leu Ser Val Phe Lys
435 440 445

Asn Leu Asp His Ser Pro Tyr Leu Phe Asn Phe His Asn Gln Glu Val
450 455 460

Lys His Lys Gly Val Leu Ala His Asn Val Ala Arg Val Val Gly His
465 470 475 480

Thr Met Ile Ile Gly Ala Thr Gly Ala Gly Lys Thr Thr Leu Ile Ser
485 490 495

Tyr Leu Met Met Ser Ala Leu Lys Tyr Ser Asn Ile Asp Ile Leu Ala
500 505 510

Leu Asp Arg Leu Asn Gly Leu Tyr Ser Phe Thr Lys Tyr Phe Asp Gly
515 520 525

Ile Tyr Asn Gln Gly Glu Asn Phe His Ile Asn Pro Phe Ser Leu Glu
530 535 540

Asp Ser Ala Thr Asn Arg Ala Phe Leu Leu His Phe Tyr Ala Gln Met
545 550 555 560

Ala Lys Val Asp Ser Tyr Asp Asp His Lys Asp Lys Val Glu Asp Arg
565 570 575

Thr Ala Leu Leu Asn Ala Ile Asp Thr Met Tyr Arg Asn Tyr Asn Asp
580 585 590

Glu Val Lys Gln Ala Lys Phe Ser Asn Gln Glu Leu Pro Leu Pro Phe
595 600 605

Asp Leu Lys Glu Phe Val Asn Ala Ile Ala Lys Thr Asn Thr Asp Ile
610 615 620

Leu Asp Ser Ser Phe Glu Asp Tyr Leu Lys Ser Ser Leu Phe Ser Ser
625 630 635 640

Arg Met Asp Ser Leu Asp Phe Lys Thr Arg Ile Ser Thr Ile Asn Thr
645 650 655

Asp Ser Ile Leu His Asn Asp Asp Asp Ala Gly Leu Leu Ala Tyr Tyr
660 665 670

Val Phe His Lys Met Ile Asp Arg Ala Leu Lys Ile Asn Arg Gly Phe
675 680 685

Leu Cys Phe Ile Asp Glu Phe Lys Ser Tyr Ala Gln Asn Glu Met Met
690 695 700

Asn Lys Lys Ile Asn Glu Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly
705 710 715 720

Val Ile Val Leu Ala Leu Gln Asp Ile Asn Gln Leu Ser Glu Val Arg
725 730 735

Asn Ala Gln Ser Phe Ile Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro
740 745 750

Gln Arg Asn Ile Asp Thr Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg
755 760 765

Leu Ser Asp Thr Glu Lys His Phe Leu Glu Asn Thr Ala Val Asn Glu
770 775 780

Tyr Lys Val Leu Leu Lys Asn Met Asn Asp Gly Ser Ser Asn Ile Ile
785 790 795 800

Asp Val Ser Leu Ser Ser Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser
805 810 815

Asn Ser Ser Met Val Glu His Ile Asp Asn Leu Ile Lys His Tyr Pro
820 825 830

Lys Thr Trp Arg Glu Val Phe Val Ser Asn Lys His Glu Asn Phe Asp
835 840 845

Asp Lys Lys His Leu Glu Lys Val Leu Lys
850 855

<210> 221

<211> 599

<212> PRT

<213> Helicobacter pylori

<400> 221

Met Lys Asn Ile Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly
1 5 10 15

Lys Thr Thr Leu Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser
20 25 30

Glu Arg Glu Lys Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu
35 40 45

Arg Glu Arg Gly Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr
50 55 60

Lys Asp Thr Lys Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe
65 70 75 80

Gly Gly Glu Val Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu
85 90 95

Leu Val Asp Ala Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val
100 105 110

Lys Lys Ala Leu Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys
115 120 125

Ile Asp Lys Pro Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe
130 135 140

Asp Leu Phe Val Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro
145 150 155 160

Val Val Tyr Ala Ala Ala Arg Asp Gly Tyr Ala Met Lys Ser Leu Asp
165 170 175

Asp Glu Lys Lys Asn Leu Glu Pro Leu Phe Glu Thr Ile Leu Glu His
180 185 190

Val Pro Ser Pro Ser Gly Ser Val Asp Glu Pro Leu Gln Met Gln Ile
195 200 205

Phe Thr Leu Asp Tyr Asp Asn Tyr Val Gly Lys Ile Gly Ile Ala Arg
210 215 220

Val Phe Asn Gly Ser Val Lys Lys Asn Glu Ser Val Leu Leu Met Lys
225 230 235 240

Ser Asp Gly Ser Lys Glu Asn Gly Arg Ile Thr Lys Leu Ile Gly Phe
245 250 255

Leu Gly Leu Ala Arg Thr Glu Ile Glu Asn Ala Tyr Ala Gly Asp Ile
260 265 270

Val Ala Ile Ala Gly Phe Asn Ala Met Asp Val Gly Asp Ser Val Val
275 280 285

Asp Pro Ala Asn Pro Met Pro Leu Asp Pro Met His Leu Glu Glu Pro
290 295 300

Thr Met Ser Val Tyr Phe Ala Val Asn Asp Ser Pro Leu Ala Gly Leu
305 310 315 320

Glu Gly Lys His Val Thr Ala Asn Lys Leu Lys Asp Arg Leu Leu Lys
325 330 335

Glu Met Gln Thr Asn Ile Ala Met Lys Cys Glu Glu Met Gly Glu Gly
340 345 350

Lys Phe Lys Val Ser Gly Arg Gly Glu Leu Gln Ile Thr Ile Leu Ala
355 360 365

Glu Asn Leu Arg Arg Glu Gly Phe Glu Phe Ser Ile Ser Arg Pro Glu
370 375 380

Val Ile Ile Lys Glu Glu Asn Gly Val Lys Cys Glu Pro Phe Glu His
385 390 395 400

Leu Val Ile Asp Thr Pro Gln Asp Phe Ser Gly Ala Ile Ile Glu Arg
405 410 415

Leu Gly Lys Arg Lys Ala Glu Met Lys Ala Met Asn Pro Met Ser Asp
420 425 430

Gly Tyr Thr Arg Leu Glu Phe Glu Ile Pro Ala Arg Gly Leu Ile Gly
435 440 445

Tyr Arg Ser Glu Phe Leu Thr Asp Thr Lys Gly Glu Gly Val Met Asn
    450   455   460

His Ser Phe Leu Glu Phe Arg Pro Phe Ser Gly Ser Val Glu Ser Arg
465   470   475   480

Lys Asn Gly Ala Leu Ile Ser Met Glu Asn Gly Glu Ala Thr Ala Phe
                485   490   495

Ser Leu Phe Asn Ile Gln Glu Arg Gly Thr Leu Phe Ile Asn Pro Gln
            500   505   510

Thr Lys Val Tyr Val Gly Met Val Ile Gly Glu His Ser Arg Asp Asn
        515   520   525

Asp Leu Asp Val Asn Pro Ile Lys Ser Lys His Leu Thr Asn Met Arg
    530   535   540

Ala Ser Gly Ser Asp Asp Ala Ile Lys Leu Thr Pro Pro Arg Thr Met
545   550   555   560

Val Leu Glu Arg Ala Leu Glu Trp Ile Glu Glu Asp Glu Ile Leu Glu
                565   570   575

Val Thr Pro Leu Asn Leu Arg Ile Arg Lys Lys Ile Leu Asp Pro Asn
            580   585   590

Met Arg Lys Arg Ala Lys Lys
        595

<210> 222

<211> 314

<212> PRT

<213> Helicobacter pylori

<400> 222

Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser Leu Gly Phe
1   5   10   15

Leu Lys Ala His Glu Val Ser Ala Glu Glu Ile Ala Asp Ile Phe Tyr
            20   25   30

Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His Thr Lys Gly
        35   40   45

Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Ala Gln Ala Lys Lys Asp
    50   55   60

Leu Asp Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala Ser Val Arg
65 70 75 80

Tyr Ser Leu Gly Gly Val Ala Met Asp Asp Lys Ser Lys Val Arg Gly
85 90 95

Met Ala Leu Lys Leu Glu Asn Gln Asn Ala Ser Trp Thr Met Val Met
100 105 110

Leu Asn Thr Glu Ile Asn Phe Ala Lys Asn Pro Asn Glu Phe Ala Gln
115 120 125

Phe Phe Glu Met Arg Ile Pro Lys Asn Gly Lys Val Asp Glu Ala Arg
130 135 140

Ile Lys Lys Leu Tyr Glu Glu Val Pro Ser Tyr Arg Asn Phe Ala Ala
145 150 155 160

Tyr Thr Lys Thr Ile Gly Ile Ser Ser Ser Val Ala Asn Thr Pro Tyr
165 170 175

Tyr Ser Val His Ala Phe Arg Phe Lys Asp Lys Lys Gly Lys Leu Leu
180 185 190

Pro Ala Arg Trp Lys Phe Val Pro Lys Glu Gly Ile Lys Tyr Leu Asn
195 200 205

Pro Gln Glu Leu Lys Gln Lys Asp Ser Asn Tyr Leu Leu Ser Ala Phe
210 215 220

Gln Gln His Leu Lys Thr Lys Pro Ile Glu Tyr Gln Met Tyr Leu Val
225 230 235 240

Phe Ala Asn Lys Asn Asp Ala Thr Asn Asp Thr Thr Ala Leu Trp Lys
245 250 255

Gly Lys His Lys Glu Leu Leu Val Gly Thr Leu Lys Val Glu Lys Tyr
260 265 270

Glu Gly Met Gly Cys Asn Lys Asp Val Tyr Phe Pro Ala Asp Leu Pro
275 280 285

Lys Gly Val Glu Ala Pro Thr Asp Pro Leu Phe Gln Ile Arg Asn Glu
290 295 300

Val Tyr Gly Ile Thr Phe Ser Arg Arg Gln
305 310

<210> 223

<211> 452

<212> PRT

<213> Helicobacter pylori

<400> 223

Met Leu Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu
1 5 10 15

Gln Ser Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val
20 25 30

Asp Leu Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val
35 40 45

Gly Glu Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val
50 55 60

Asn Ser Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala
65 70 75 80

Lys Phe Arg Ala Phe Glu Ser Met Lys Gln Arg His Leu Pro Thr Pro
85 90 95

Arg Met Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn
100 105 110

Asn Gln Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile
115 120 125

Arg Ala Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val
130 135 140

Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala
145 150 155 160

Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr
165 170 175

Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu
180 185 190

Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg
195 200 205

Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser
210 215 220

Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu
225 230 235 240

Lys Arg Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser
245 250 255

Arg Glu Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys
260 265 270

Lys Ala Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn
275 280 285

Tyr Gln Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr
290 295 300

Leu Arg Asp Glu Arg Lys Lys Ala Lys Ala Thr Lys Lys Ala Met Glu
305 310 315 320

Phe Glu Glu Arg Glu Lys Glu His Asp Glu Arg Asp Glu Gln Glu Thr
325 330 335

Glu Gly Arg Arg Lys Ala Leu Glu Met Asp Lys Gly Asp Lys Lys Glu
340 345 350

Glu Arg Val Lys Pro Lys Glu Asn Glu Arg Glu Ile Lys Gln Glu Ala
355 360 365

Ile Lys Glu Pro Ser Asp Gly Asn Asn Ala Thr Gln Gln Gly Glu Lys
370 375 380

Gln Asn Ala Pro Lys Glu Asn Asn Ala Gln Lys Glu Glu Asn Lys Pro
385 390 395 400

Asn Ser Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala
405 410 415

Lys Ala Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala Arg Glu His
420 425 430

Gln Glu Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu
435 440 445

Ala Gly Lys Lys
450

<210> 224

<211> 276

<212> PRT

<213> Helicobacter pylori

<400> 224

Met Phe Lys Asp Phe Tyr Arg Thr Thr Leu Ser Phe Leu Lys Pro Leu
1   5   10   15

Leu Leu Leu Leu Val Leu Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp
            20   25   30

Glu Tyr Ile Ser Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His
        35   40   45

Lys Thr Tyr Tyr Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln
    50   55   60

Tyr Gln Gln Ala Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile
65   70   75   80

Gly Leu Gly Ser Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly
                85   90   95

Val Lys Val Asp Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile
            100   105   110

Lys Gly Tyr Gly Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg
        115   120   125

Met Gln Ala Glu Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu
    130   135   140

Lys Thr Tyr Arg His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn
145   150   155   160

Phe Ala Asn Asn Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met
                165   170   175

Leu Ile Gly Ser Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro
            180   185   190

Ile Lys Phe Gly Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln
        195   200   205

Ile Lys Asp Lys Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser
    210   215   220

Asn Ile Thr Leu Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg Ile
225   230   235   240

Gly Ile Ala Tyr Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg
                245   250   255

Ala Lys Lys Phe Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala
            260   265   270

Met Glu Ala Leu
275

<210> 225

<211> 330

<212> PRT

<213> Helicobacter pylori

<400> 225

Met Thr Glu Asp Arg Leu Ser Ala Glu Asp Lys Lys Phe Leu Glu Val
1 5 10 15

Glu Arg Ala Leu Lys Glu Ala Ala Leu Asn Pro Leu Arg His Ala Thr
20 25 30

Glu Glu Leu Phe Gly Asp Phe Leu Lys Met Glu Asn Ile Thr Glu Ile
35 40 45

Cys Tyr Asn Gly Asn Lys Val Val Trp Val Leu Lys Asn Asn Gly Glu
50 55 60

Trp Gln Pro Phe Asp Val Arg Asp Arg Lys Ala Phe Ser Leu Ser Arg
65 70 75 80

Leu Met His Phe Ala Arg Cys Cys Ala Ser Phe Lys Lys Lys Thr Ile
85 90 95

Asp Asn Tyr Glu Asn Pro Ile Leu Ser Ser Asn Leu Ala Asn Gly Glu
100 105 110

Arg Val Gln Ile Val Leu Ser Pro Val Thr Val Asn Asp Glu Thr Ile
115 120 125

Ser Ile Ser Ile Arg Ile Pro Ser Lys Thr Thr Tyr Pro His Ser Phe
130 135 140

Phe Glu Glu Gln Gly Phe Tyr Asn Leu Leu Asp Asn Lys Glu Gln Ala
145 150 155 160

Ile Ser Ala Ile Lys Asp Gly Ile Ala Ile Gly Lys Asn Val Ile Val
165 170 175

Cys Gly Gly Thr Gly Ser Gly Lys Thr Thr Tyr Ile Lys Ser Ile Met
180 185 190

Glu Phe Ile Pro Lys Glu Glu Arg Ile Ile Ser Ile Glu Asp Thr Glu
195 200 205

Glu Ile Val Phe Lys His His Lys Asn Tyr Thr Gln Leu Phe Phe Gly
    210   215   220

Gly Asn Ile Thr Ser Ala Asp Cys Leu Lys Ser Cys Leu Arg Met Arg
225   230   235   240

Pro Asp Arg Ile Ile Leu Gly Glu Leu Arg Ser Ser Glu Ala Tyr Asp
                245   250   255

Phe Tyr Asn Val Leu Cys Ser Gly His Lys Gly Thr Leu Thr Thr Leu
            260   265   270

His Ala Gly Ser Ser Glu Glu Ala Phe Ile Arg Leu Ala Asn Met Ser
        275   280   285

Ser Ser Asn Ser Ala Ala Arg Asn Ile Lys Phe Glu Ser Leu Ile Glu
    290   295   300

Gly Phe Lys Asp Leu Ile Asp Met Ile Val His Ile Asn His His Lys
305   310   315   320

Gln Cys Asp Glu Phe Tyr Ile Lys His Arg
                325   330

<210> 226

<211> 1927

<212> PRT

<213> Helicobacter pylori

<220>

<221> MISC_FEATURE

<222> (907)..(907)

<223> "X" can be any amino acid

<400> 226

Met Asn Glu Glu Asn Asp Lys Leu Glu Thr Ser Lys Lys Ala Gln Gln
1   5   10   15

Asp Ser Pro Gln Asp Leu Ser Asn Glu Glu Ala Thr Glu Ala Asn His
            20   25   30

Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser Asp His His Leu
        35   40   45

Asp Asn Pro Thr Glu Thr Gln Thr His Phe Asp Gly Asp Lys Ser Glu
50 55 60

Glu Thr Gln Thr Gln Met Asp Ser Glu Gly Asn Glu Thr Ser Glu Ser
65 70 75 80

Ser Asn Gly Ser Leu Ala Asp Lys Leu Phe Lys Lys Ala Arg Lys Leu
85 90 95

Val Asp Asn Lys Lys Pro Phe Thr Gln Gln Lys Asn Leu Asp Glu Glu
100 105 110

Thr Gln Glu Leu Asn Glu Glu Asp Asp Gln Glu Asn Asn Glu Tyr Gln
115 120 125

Glu Glu Thr Gln Thr Asp Leu Ile Asp Asp Glu Thr Ser Lys Lys Thr
130 135 140

Gln Gln His Ser Pro Gln Asp Leu Ser Asn Glu Glu Ala Thr Glu Ala
145 150 155 160

Asn His Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser Asp His
165 170 175

His Leu Asp Asn Pro Thr Glu Thr Gln Thr Asn Phe Asp Gly Asp Lys
180 185 190

Ser Glu Glu Thr Gln Thr Gln Met Asp Ser Glu Gly Asn Glu Thr Ser
195 200 205

Glu Ser Ser Asn Gly Ser Leu Ala Asp Lys Leu Phe Lys Lys Ala Arg
210 215 220

Lys Leu Val Asp Asn Lys Lys Pro Phe Thr Gln Gln Lys Asn Leu Asp
225 230 235 240

Glu Glu Thr Gln Glu Leu Asn Glu Glu Asp Asp Gln Glu Asn Asn Glu
245 250 255

Tyr Gln Glu Glu Thr Gln Thr Asp Leu Ile Asp Asp Glu Thr Ser Lys
260 265 270

Lys Thr Gln Gln His Ser Pro Gln Asp Leu Ser Asn Glu Glu Ala Thr
275 280 285

Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser
290 295 300

Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr Asn Phe Asp Gly
305 310 315 320

Asp Lys Ser Glu Glu Ile Thr Asp Asp Ser Asn Asp Gln Glu Ile Ile
325 330 335

Lys Gly Ser Lys Lys Lys Tyr Ile Ile Gly Gly Ile Val Val Ala Val
340 345 350

Leu Ile Val Ile Ile Leu Phe Ser Arg Ser Ile Phe His Tyr Phe Met
355 360 365

Pro Leu Glu Asp Lys Ser Ser Arg Phe Ser Lys Asp Arg Asn Leu Tyr
370 375 380

Val Asn Asp Glu Ile Gln Ile Arg Gln Glu Tyr Asn Arg Leu Leu Lys
385 390 395 400

Glu Arg Asn Glu Lys Gly Asn Met Ile Asp Lys Asn Leu Phe Phe Asn
405 410 415

Asp Asp Pro Asn Arg Thr Leu Tyr Asn Tyr Leu Asn Ile Ala Glu Ile
420 425 430

Glu Asp Lys Asn Pro Leu Arg Ala Phe Tyr Glu Cys Ile Ser Asn Gly
435 440 445

Gly Asn Tyr Glu Glu Cys Leu Lys Leu Ile Lys Asp Lys Lys Leu Gln
450 455 460

Asp Gln Met Lys Lys Thr Leu Glu Ala Tyr Asn Asp Cys Ile Lys Asn
465 470 475 480

Ala Lys Thr Glu Glu Glu Arg Ile Lys Cys Leu Asp Leu Ile Lys Asp
485 490 495

Glu Asn Leu Lys Lys Ser Leu Leu Asn Gln Gln Lys Val Gln Val Ala
500 505 510

Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu Glu Arg Asn Glu Cys
515 520 525

Leu Lys Leu Ile Asn Asp Pro Glu Ile Arg Glu Lys Phe Arg Lys Glu
530 535 540

Leu Glu Leu Gln Lys Glu Leu Gln Glu Tyr Lys Asp Cys Ile Lys Asn
545 550 555 560

Ala Lys Thr Glu Ala Glu Lys Asn Lys Cys Leu Lys Gly Leu Ser Lys
565 570 575

Glu Ala Ile Glu Arg Leu Lys Gln Gln Ala Leu Asp Cys Leu Lys Asn
580 585 590

Ala Lys Thr Asp Glu Glu Arg Asn Glu Cys Leu Lys Asn Ile Pro Gln
595 600 605

Asp Leu Gln Lys Glu Leu Leu Ala Asp Met Ser Val Lys Ala Tyr Lys
610 615 620

Asp Cys Val Ser Lys Ala Arg Asn Glu Lys Glu Lys Gln Glu Cys Glu
625 630 635 640

Lys Leu Leu Thr Pro Glu Ala Arg Lys Lys Leu Glu Gln Gln Val Leu
645 650 655

Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu Glu Arg Lys Lys Cys Leu
660 665 670

Lys Asp Leu Pro Lys Asp Leu Gln Ser Asp Ile Leu Ala Lys Glu Ser
675 680 685

Leu Lys Ala Tyr Lys Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu
690 695 700

Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Leu Leu
705 710 715 720

Glu Glu Glu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser
725 730 735

Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr
740 745 750

Pro Glu Ala Lys Lys Lys Leu Glu Glu Ala Lys Lys Ser Val Lys Ala
755 760 765

Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu
770 775 780

Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Gln Gln
785 790 795 800

Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Lys Glu Arg Lys Lys
805 810 815

Cys Leu Lys Asp Leu Pro Lys Asp Leu Gln Lys Lys Val Leu Ala Lys
820 825 830

Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Gln Ala Lys Thr Glu
835 840 845

Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys
850 855 860

Leu Leu Glu Glu Ala Lys Lys Ser Val Lys Ala Tyr Leu Asp Cys Val
865 870 875 880

Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu
885 890 895

Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Xaa Ala Lys Glu Ser Val
900 905 910

Lys Ala Tyr Leu Asp Cys Val Ser Gln Ala Lys Asn Glu Ala Glu Lys
915 920 925

Lys Glu Cys Glu Lys Leu Leu Thr Leu Glu Ser Lys Lys Lys Leu Glu
930 935 940

Glu Ala Lys Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Gln Ala
945 950 955 960

Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu
965 970 975

Ala Lys Lys Leu Leu Glu Gln Gln Ala Leu Asp Cys Leu Lys Asn Ala
980 985 990

Lys Thr Glu Ala Asp Lys Lys Arg Cys Val Lys Asp Leu Pro Lys Asp
995 1000 1005

Leu Gln Lys Lys Val Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys
1010 1015 1020

Asp Cys Val Ser Lys Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys
1025 1030 1035

Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala
1040 1045 1050

Lys Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Gln Ala Lys
1055 1060 1065

Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu
1070 1075 1080

Ala Arg Lys Leu Leu Glu Glu Ala Lys Glu Ser Val Lys Ala Tyr
1085 1090 1095

Lys Asp Cys Val Ser Lys Ala Arg Asn Glu Lys Glu Lys Lys Glu
1100 1105 1110

Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Gln
1115 1120 1125

Gln Val Leu Asp Cys Leu Lys Asn Ala Lys Thr Glu Ala Asp Lys
1130 1135 1140

Lys Arg Cys Val Lys Asp Leu Pro Lys Asp Leu Gln Lys Lys Val
1145 1150 1155

Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg
1160 1165 1170

Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr
1175 1180 1185

Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu Lys
1190 1195 1200

Ala Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg
1205 1210 1215

Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu
1220 1225 1230

Glu Gln Glu Val Lys Lys Ser Ile Lys Ala Tyr Leu Asp Cys Val
1235 1240 1245

Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu
1250 1255 1260

Leu Thr Pro Glu Ala Arg Lys Phe Leu Ala Lys Gln Val Leu Asn
1265 1270 1275

Cys Leu Glu Lys Ala Gly Asn Glu Glu Glu Arg Lys Ala Cys Leu
1280 1285 1290

Lys Asn Leu Pro Lys Asp Leu Gln Glu Asn Ile Leu Ala Lys Glu
1295 1300 1305

Ser Leu Lys Ala Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu
1310 1315 1320

Glu Glu Arg Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg
1325 1330 1335

Lys Leu Leu Glu Gln Glu Val Lys Lys Ser Val Lys Ala Tyr Leu
1340 1345 1350

Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys
1355 1360 1365

Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu Ala Lys Glu
1370 1375 1380

Leu Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys Leu Lys Asn Ala
1385 1390 1395

Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu Asp Gly Leu
1400 1405 1410

Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg Glu Lys
1415 1420 1425

Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu Lys
1430 1435 1440

Arg Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln
1445 1450 1455

Asn Lys Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu
1460 1465 1470

Arg Leu His Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro
1475 1480 1485

Thr Asp Gln Glu Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp
1490 1495 1500

Ser Glu Arg Ala Leu Ile Leu Gly Ile Lys Arg Gln Ala Asp Glu
1505 1510 1515

Val Asp Leu Ile Tyr Ser Asp Leu Arg Asn Arg Lys Thr Phe Asp
1520 1525 1530

Asn Met Ala Ala Lys Gly Tyr Pro Leu Leu Pro Met Asp Phe Lys
1535 1540 1545

Asn Gly Gly Asp Ile Ala Thr Ile Asn Ala Thr Asn Val Asp Ala
1550 1555 1560

Asp Lys Ile Ala Ser Asp Asn Pro Ile Tyr Ala Ser Ile Glu Pro
1565 1570 1575

Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys Thr Ile Lys Asp Lys
1580 1585 1590

Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly Gly Asn Lys Lys
1595 1600 1605

Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala Glu Ala Lys
1610 1615 1620

Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr Ala Lys
1625 1630 1635

Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser Gly
1640 1645 1650

Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys
1655 1660 1665

Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile
1670 1675 1680

Gly Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile
1685 1690 1695

Glu Ile Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile
1700 1705 1710

Val Ser Gly Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr
1715 1720 1725

Met Ile Leu Leu Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln
1730 1735 1740

Ser Val Lys Gly Gly Thr Pro Ile Met Thr Arg Leu Met Ile Val
1745 1750 1755

Phe Thr Lys Ala Ile Thr Pro Asp Gly Val Ile Ile Pro Leu Ala
1760 1765 1770

Asn Ala Gln Ala Ala Gly Met Leu Gly Glu Ala Gly Val Asp Gly
1775 1780 1785

Tyr Val Asn Asn His Phe Met Lys Arg Ile Gly Phe Ala Val Ile
1790 1795 1800

Ala Ser Val Val Asn Ser Phe Leu Gln Thr Ala Pro Ile Ile Ala
1805 1810 1815

Leu Asp Lys Leu Ile Gly Leu Gly Lys Gly Arg Ser Glu Arg Thr
1820 1825 1830

Pro Glu Phe Asn Tyr Ala Leu Gly Gln Ala Ile Asn Gly Ser Met
1835 1840 1845

Gln Ser Ser Ala Gln Met Ser Asn Gln Ile Leu Gly Gln Leu Met
1850 1855 1860

Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly Asp Ser Ile Lys
1865 1870 1875

Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val Tyr Asp Val
1880 1885 1890

Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys Gln Ser
1895 1900 1905

Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser Pro
1910 1915 1920

Lys Gly Gly Asn
1925

<210> 227

<211> 381

<212> PRT

<213> Helicobacter pylori

<400> 227

Val Lys Cys Phe Leu Ser Ile Phe Ser Phe Leu Thr Phe Cys Gly Leu
1 5 10 15

Ser Leu Asn Gly Thr Glu Val Val Ile Thr Leu Glu Pro Ala Leu Lys
20 25 30

Ala Ile Gln Ala Asp Ala Gln Ala Lys Gln Lys Thr Ala Gln Ala Glu
35 40 45

Leu Lys Ala Ile Glu Ala Gln Ser Ser Ala Lys Glu Lys Ala Ile Gln
50 55 60

Ala Gln Ile Glu Gly Glu Leu Arg Thr Gln Leu Ala Thr Met Ser Ala
65 70 75 80

Met Leu Lys Gly Ala Asn Gly Val Ile Asn Gly Val Asn Gly Met Thr
85 90 95

Gly Gly Phe Phe Ala Gly Ser Asp Ile Leu Leu Gly Val Met Glu Gly
100 105 110

Tyr Ser Ser Ala Leu Ser Ala Leu Gly Gly Asn Val Lys Met Ile Val
115 120 125

Glu Lys Gln Lys Ile Asn Thr Gln Thr Glu Ile Gln Asn Met Gln Ile
130 135 140

Ala Leu Gln Lys Asn Asn Glu Ile Ile Lys Leu Lys Met Asn Gln Gln
145 150 155 160

Asn Ala Leu Leu Glu Ala Leu Lys Asn Ser Phe Glu Pro Ser Val Thr
165 170 175

Leu Lys Thr Gln Met Glu Met Leu Ser Gln Ala Leu Gly Ser Ser Ser
180 185 190

Asp Asn Ala Gln Tyr Ile Ala Tyr Asn Thr Ile Gly Ile Lys Ala Phe
195 200 205

Glu Glu Thr Leu Lys Gly Phe Glu Thr Trp Leu Lys Val Ala Met Gln
210 215 220

Lys Ala Thr Leu Ile Asp Tyr Asn Ser Leu Thr Gly Gln Ala Leu Phe
225 230 235 240

Gln Ser Ala Ile Tyr Ala Pro Ala Leu Ser Phe Phe Ser Ser Met Gly
245 250 255

Ala Pro Phe Gly Ile Ile Glu Thr Phe Thr Leu Ala Pro Thr Lys Cys
260 265 270

Pro Tyr Leu Asp Gly Leu Lys Ile Ser Ala Cys Leu Met Glu Gln Val
275 280 285

Ile Gln Asn Tyr Arg Met Ile Val Ala Leu Ile Gln Asn Lys Leu Ser
290 295 300

Asp Ala Asp Phe Gln Asn Ile Ala Tyr Leu Asn Gly Ile Asn Gly Glu
305 310 315 320

Ile Lys Thr Leu Lys Gly Ser Val Asp Leu Asn Ala Leu Ile Glu Val
325 330 335

Ala Ile Leu Asn Ala Glu Asn His Leu Asn Tyr Ile Glu Asn Leu Glu
340 345 350

Lys Lys Ala Asp Leu Trp Glu Glu Gln Leu Lys Leu Glu Arg Glu Thr
355 360 365

Thr Ala Arg Asn Ile Ala Ser Ser Lys Val Ile Val Lys
370 375 380

<210> 228

<211> 370

<212> PRT

<213> Helicobacter pylori

<220>

<221> MISC_FEATURE

<222> (245)..(245)

<223> "X" can be any amino acid

<400> 228

Met Ala Gly Thr Gln Ala Ile Tyr Glu Ser Ser Ser Ala Gly Phe Leu
1 5 10 15

Ser Glu Ile Ser Ser Ile Ile Ser Ser Thr Ser Gly Val Ala Gly Pro
20 25 30

Phe Ala Gly Ile Val Ala Gly Ala Met Ser Ala Ala Ile Ile Pro Ile
35 40 45

Val Val Gly Phe Thr Asn Pro Gln Met Thr Ala Ile Met Thr Gln Tyr
50 55 60

Asn Gln Ser Ile Ala Glu Ala Val Ser Met Pro Met Lys Ala Ala Asn
65 70 75 80

Gln Gln Tyr Asn Gln Leu Tyr Gln Gly Phe Asn Asp Gln Ser Met Ala
85 90 95

Val Gly Asn Asn Ile Leu Asn Ile Ser Lys Leu Thr Gly Glu Phe Asn
100 105 110

Val Gln Gly Asn Thr Gln Gly Ala Gln Ile Ser Ala Val Asn Ser Gln
115 120 125

Ile Ala Ser Ile Leu Ala Ser Asn Thr Thr Pro Lys Asn Pro Ser Ala
130 135 140

Ile Glu Ala Tyr Ala Thr Asn Gln Ile Ala Val Pro Ser Val Pro Thr
145 150 155 160

Thr Val Glu Met Met Ser Gly Ile Leu Gly Asn Ile Thr Ser Ala Ala
165 170 175

Pro Lys Tyr Ala Leu Ala Leu Gln Glu Gln Leu Arg Ser Gln Ala Ser
180 185 190

Asn Ser Ser Met Asn Asp Thr Ala Asp Ser Leu Asp Ser Cys Thr Ala
195 200 205

Leu Gly Ala Leu Val Gly Ser Ser Lys Val Phe Phe Ser Cys Met Gln
210 215 220

Ile Ser Met Thr Pro Met Ser Val Ser Met Pro Thr Val Tyr Ala Lys
225 230 235 240

Tyr Gln Ala Leu Xaa Thr Asn Ala Leu Thr Ser Gly Thr Asn Pro Met
245 250 255

Thr Thr Pro Ala Cys Pro Ile Gly Asp Lys Val Leu Ala Val Tyr Cys
260 265 270

Tyr Ala Glu Lys Val Ala Glu Ile Leu Arg Glu Tyr Tyr Ile Glu Phe
275 280 285

Val Lys Asn Asn Thr Asn Leu Leu Gln Asn Ala Ser Gln Met Ile Leu
290 295 300

Asn Gln Ser Gly Leu Ala Thr Ser Thr Tyr Asp Thr Gln Ala Ile Ser
305 310 315 320

Asn Ile Ser Ser Leu Tyr Asn Tyr Asn Ile Val Ala Asn Lys Ser Phe
325 330 335

Leu Lys Ser His Leu Thr Tyr Leu Asp Tyr Ile Lys Asn Lys Leu Lys
340 345 350

Gly Gln Lys Asp Ser Tyr Leu Thr Glu Arg Val Gln Thr Lys Ile Ile
355 360 365

Val Lys
370

<210> 229

<211> 142

<212> PRT

<213> Helicobacter pylori

<400> 229

Met Lys Thr Asn Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu
1 5 10 15

Ile Ile Gly Met Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp
20 25 30

Ile Lys Asp Ile Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu
35 40 45

Val Ser Arg Asp Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu
50 55 60

Gln Lys Val Ala Val Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile
65 70 75 80

Lys Phe Asp Asn Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu
85 90 95

Gly Ile Asn Ala Met Trp Gly Ile Gln Asn Leu Leu Met Ser Gln Met
100 105 110

Met Gly Asp Tyr Gly Pro Asn Asn Pro Phe Met Tyr Gly Tyr Ala Pro
115 120 125

Thr Tyr Ser Asp Ser Ser Phe Leu Pro Pro Ile Leu Gly Tyr
130 135 140

<210> 230

<211> 983

<212> PRT

<213> Helicobacter pylori

<400> 230

Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1 5 10 15

Glu Gln Glu Val Gln Lys Arg Gln Phe Lys Lys Ile Glu Glu Leu Lys
20 25 30

Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
35 40 45

Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
50 55 60

Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65 70 75 80

Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
85 90 95

Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
100 105 110

Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
115 120 125

Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
130 135 140

Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145 150 155 160

Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
165 170 175

Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
180 185 190

Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
195 200 205

Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
210 215 220

Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225 230 235 240

Tyr Ser Leu Ile Phe Ser Asn Asp Phe Met Arg Ala Tyr Asn Glu Lys
245 250 255

Gln Lys Arg Glu Ser Phe Tyr Asp Ile Ser Phe Tyr Leu Thr Ile Glu
260 265 270

Gln Asp Leu Leu Asp Thr Leu Asn Glu Pro Val Met Asn Lys Lys His
275 280 285

Phe Ala Asp Asn Asn Phe Glu Glu Phe Gln Arg Ile Ile Arg Ala Lys
290 295 300

Leu Glu Asn Phe Lys Asp Arg Ile Glu Leu Ile Glu Glu Leu Leu Ser
305 310 315 320

Lys Tyr His Pro Ile Arg Leu Lys Glu Tyr Thr Lys Asp Gly Val Ile
325 330 335

Tyr Ser Lys Gln Cys Glu Phe Tyr Asn Phe Leu Val Gly Met Asn Glu
340 345 350

Ala Pro Phe Ile Cys Asn Arg Lys Asp Leu Tyr Leu Lys Glu Lys Met
355 360 365

His Gly Gly Val Lys Glu Val Tyr Phe Ala Asn Lys His Gly Lys Ile
370 375 380

Leu Asn Asp Asp Leu Ser Glu Lys Tyr Phe Ser Ala Ile Glu Ile Ser
385 390 395 400

Glu Tyr Ala Pro Lys Ser Gln Ser Asp Leu Phe Asp Lys Ile Asn Ala
405 410 415

Leu Asp Ser Glu Phe Ile Phe Met His Ala Tyr Ser Pro Lys Asn Ser
420 425 430

Gln Val Leu Lys Asp Lys Leu Ala Phe Thr Ser Arg Arg Ile Ile Ile
435 440 445

Ser Gly Gly Ser Lys Glu Gln Gly Met Thr Leu Gly Cys Leu Ser Glu
450 455 460

Leu Val Gly Asn Gly Asp Ile Thr Leu Gly Ser Tyr Gly Asn Ser Leu
465 470 475 480

Val Leu Phe Ala Asp Ser Phe Glu Lys Met Lys Gln Ser Val Lys Glu
485 490 495

Cys Val Ser Ser Leu Asn Ala Lys Gly Phe Leu Ala Asn Ala Ala Thr
500 505 510

Phe Ser Met Glu Asn Tyr Phe Phe Ala Lys His Cys Ser Phe Ile Thr
515 520 525

Leu Pro Phe Ile Phe Asp Val Thr Ser Asn Asn Phe Ala Asp Phe Ile
530 535 540

Ala Met Arg Ala Met Ser Phe Asp Gly Asn Gln Glu Asn Asn Ala Trp
545 550 555 560

Gly Asn Ser Val Met Thr Leu Lys Ser Glu Ile Asn Ser Pro Phe Tyr
565 570 575

Leu Asn Phe His Met Pro Thr Asp Phe Gly Ser Ala Ser Ala Gly His
580 585 590

Thr Leu Ile Leu Gly Ser Thr Gly Ser Gly Lys Thr Val Phe Met Ser
595 600 605

Met Thr Leu Asn Ala Met Gly Gln Phe Val His Asn Phe Pro Ala Asn
610 615 620

Val Ser Lys Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp
625 630 635 640

Tyr Gly Ala Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys
645 650 655

Ile Glu Leu Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala
660 665 670

Cys Val Gln Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile
675 680 685

Ser Val Val Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu
690 695 700

Lys Asp Glu Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn
705 710 715 720

Thr Leu Ala Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu
725 730 735

Asp Tyr Pro Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn
740 745 750

Asp Pro Asn Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr
755 760 765

Asn Gly Glu Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu
770 775 780

Asp Phe Ser Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp
785 790 795 800

Asn Asn Asp Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile
805 810 815

Gln Glu Ala Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala
820 825 830

Trp Lys Tyr Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met
835 840 845

Leu Lys Thr Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln
850 855 860

Ser Ile Thr Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu
865 870 875 880

Gln Cys Pro Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser
885 890 895

Asp Tyr Gln Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile
900 905 910

Thr Lys Gly Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro
915 920 925

Ser Val Ile Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu
930 935 940

Lys Ile Leu Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile
945 950 955 960

Ile Gln Asn His Ser Ile Ile Asp Lys Tyr Gln Ala Leu Arg Gln Met
965 970 975

Tyr Gln Gln Ile Lys Glu Tyr
980

<210> 231

<211> 207

<212> PRT

<213> Helicobacter pylori

<400> 231

Leu Ile Asn Asn Asn Ser Asn Lys Lys Leu Arg Gly Phe Phe Val Lys
1   5   10   15

Val Leu Leu Ser Leu Val Val Phe Ser Ser Tyr Gly Leu Ala Asn Asp
            20   25   30

Asp Lys Glu Ala Lys Lys Glu Val Leu Glu Lys Glu Lys Asn Thr Pro
        35   40   45

Asn Gly Leu Val Tyr Thr Asn Leu Asp Phe Asp Ser Phe Lys Ala Thr
    50   55   60

Ile Lys Asn Leu Lys Asp Lys Lys Val Thr Phe Lys Glu Val Asn Pro
65   70   75   80

Asp Ile Ile Lys Asp Glu Val Phe Asp Phe Val Ile Val Asn Arg Val
                85   90   95

Leu Lys Lys Ile Lys Asp Leu Lys His Tyr Asp Pro Val Ile Glu Lys
            100   105   110

Ile Phe Asp Glu Lys Gly Lys Glu Met Gly Leu Asn Val Glu Leu Gln
        115   120   125

Ile Asn Pro Glu Val Lys Asp Phe Phe Thr Phe Lys Ser Ile Ser Thr
    130   135   140

Thr Asn Lys Gln Arg Cys Phe Leu Ser Leu Arg Gly Glu Thr Arg Glu
145   150   155   160

Ile Leu Cys Asp Asp Lys Leu Tyr Asn Val Leu Leu Ala Val Phe Asn
                165   170   175

Ser Tyr Asp Pro Asn Asp Leu Leu Lys His Ile Ser Thr Val Glu Ser
            180   185   190

Leu Lys Lys Ile Phe Tyr Thr Ile Thr Cys Glu Ala Val Tyr Leu
        195   200   205

<210> 232

<211> 1186

<212> PRT

<213> Helicobacter pylori

<400> 232

Met Thr Asn Glu Thr Ile Asp Gln Thr Arg Thr Pro Asp Gln Thr Gln
1 5 10 15

Ser Gln Thr Ala Phe Asp Pro Gln Gln Phe Ile Asn Asn Leu Gln Val
20 25 30

Ala Phe Ile Lys Val Asp Asn Val Val Ala Ser Phe Asp Pro Asp Gln
35 40 45

Lys Pro Ile Val Asp Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Asp
50 55 60

Gly Ile Ser Gln Leu Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn
65 70 75 80

Pro Thr Lys Lys Asn Gln Tyr Phe Ser Asp Phe Ile Asp Lys Ser Asn
85 90 95

Asp Leu Ile Asn Lys Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys
100 105 110

Ser Phe Gln Lys Phe Gly Asp Gln Arg Tyr Gln Ile Phe Thr Ser Trp
115 120 125

Val Ser His Gln Lys Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg
130 135 140

Asn Phe Met Glu Asn Ile Ile Gln Pro Pro Ile Pro Asp Asp Lys Glu
145 150 155 160

Lys Ala Glu Phe Leu Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile
165 170 175

Ile Gly Asn Gln Ile Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp
180 185 190

Glu Ser Leu Lys Glu Arg Gln Glu Ala Glu Lys Asn Gly Gly Pro Thr
195 200 205

Gly Gly Asp Trp Leu Asp Ile Phe Leu Ser Phe Ile Phe Asn Lys Lys
210 215 220

Gln Ser Ser Asp Val Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His
225 230 235 240

Val Gln Pro Asp Ile Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro
245 250 255

Pro Glu Ala Arg Asp Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe
260 265 270

Thr Leu Gly Asp Met Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile
275 280 285

Asp Pro Asn Tyr Lys Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu
290 295 300

Ser Ser Val Leu Met Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val
305 310 315 320

Ser Leu Leu Tyr Ala Gly Asn Gly Gly Phe Gly Asp Lys His Asp Trp
325 330 335

Asn Ala Thr Val Gly Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr
340 345 350

Leu Ile Asn Val His Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly
355 360 365

Gly Glu Lys Gly Ile Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp
370 375 380

Gln Leu Thr Gly Ser Gln Arg Ala Leu Ser Gln Glu Glu Ile Arg Asn
385 390 395 400

Lys Val Asp Phe Met Glu Phe Leu Ala Gln Asn Asn Thr Lys Leu Asp
405 410 415

Asn Leu Ser Glu Lys Glu Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp
420 425 430

Phe Gln Lys Asp Ser Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg
435 440 445

Ile Ala Phe Val Ser Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr
450 455 460

Glu Phe Asn Asn Gly Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys
465 470 475 480

Lys Ala Asp Lys Ala Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly
485 490 495

Ser Leu Lys His Asp Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys
500 505 510

Tyr Thr Asn Ala Ser Lys Asn Pro Asn Lys Gly Val Gly Ala Thr Asn
515 520 525

Gly Val Ser His Leu Glu Ala Gly Phe Asn Lys Val Ala Val Phe Asn
530 535 540

Leu Pro Asp Leu Asn Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn
545 550 555 560

Leu Glu Asn Lys Leu Thr Ala Lys Gly Leu Ser Leu Gln Glu Ala Asn
565 570 575

Lys Leu Ile Lys Asp Phe Leu Ser Ser Asn Lys Glu Leu Ala Gly Lys
580 585 590

Ala Leu Asn Phe Asn Lys Ala Val Ala Glu Ala Lys Ser Thr Gly Asn
595 600 605

Tyr Asp Glu Val Lys Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg
610 615 620

Lys Arg Glu His Leu Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys
625 630 635 640

Ser Gly Asn Lys Asn Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln
645 650 655

Lys Asp Glu Ile Phe Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala
660 665 670

Arg Ala Ile Ala Tyr Thr Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu
675 680 685

Ser Asp Lys Leu Glu Lys Ile Ser Lys Asp Leu Lys Asp Phe Ser Lys
690 695 700

Ser Phe Asp Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala
705 710 715 720

Glu Glu Thr Leu Lys Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile
725 730 735

Asn Pro Glu Trp Ile Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn
740 745 750

Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala
755 760 765

Lys Ser Asp Leu Glu Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys
770 775 780

Val Thr Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys
785 790 795 800

Ala Met Gly Asp Phe Ser Arg Val Glu Gln Val Leu Ala Asp Leu Lys
805 810 815

Asn Phe Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp
820 825 830

Phe Asn Thr Gly Lys Asn Ser Glu Leu Tyr Gln Ser Val Lys Asn Ser
835 840 845

Val Asn Lys Thr Leu Val Gly Asn Gly Leu Ser Gly Ile Glu Ala Thr
850 855 860

Ala Leu Ala Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Glu Lys
865 870 875 880

Phe Lys Asn Phe Asn Asn Asn Asn Asn Gly Leu Lys Asn Ser Thr Glu
885 890 895

Pro Ile Tyr Ala Lys Val Asn Lys Lys Lys Thr Gly Gln Val Ala Ser
900 905 910

Pro Glu Glu Pro Ile Tyr Thr Gln Val Ala Lys Lys Val Asn Ala Lys
915 920 925

Ile Asp Arg Leu Asn Gln Ile Ala Ser Gly Leu Gly Gly Val Gly Gln
930 935 940

Ala Ala Gly Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser
945 950 955 960

Lys Val Gly Leu Ser Ala Ser Pro Glu Pro Ile Tyr Ala Thr Ile Asp
965 970 975

Asp Leu Gly Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp
980 985 990

Leu Ser Lys Val Gly Arg Ser Arg Asn Gln Glu Leu Ala Gln Lys Ile
995 1000 1005

Asp Asn Leu Asn Gln Ala Val Ser Glu Ala Lys Ala Gly Phe Phe
1010 1015 1020

Gly Asn Leu Glu Gln Thr Ile Asp Lys Leu Lys Asp Ser Thr Lys
1025 1030 1035

Lys Asn Val Met Asn Leu Tyr Val Glu Ser Ala Lys Lys Val Pro
1040 1045 1050

Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala Ile Asn Ser His
1055 1060 1065

Thr Arg Ile Asn Ser Asn Ile Gln Asn Gly Ala Ile Asn Glu Lys
1070 1075 1080

Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu Lys Leu
1085 1090 1095

Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Ser Leu
1100 1105 1110

Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
1115 1120 1125

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val
1130 1135 1140

Lys Asp Ile Lys Ser Gly Phe Thr His Phe Leu Ala Asn Ala Phe
1145 1150 1155

Ser Thr Gly Tyr Tyr Cys Leu Ala Arg Glu Asn Ala Glu His Gly
1160 1165 1170

Ile Lys Asn Val Asn Thr Lys Gly Gly Phe Gln Lys Ser
1175 1180 1185

<210> 233

<211> 416

<212> PRT

<213> Helicobacter pylori

<400> 233

Val Ala Ile Asn Thr Phe Leu Lys His Ser Phe Leu Val Cys Leu Leu
1 5 10 15

Ala Val Asn Ser Tyr Ala Phe Asp Trp Asn Ile Phe Lys Tyr Asn Leu
20 25 30

Gly Phe Asn Met Phe Ile Met Asp His Glu Gly Ser Thr Pro Tyr Trp
35 40 45

Val Asn Thr Asn Thr Asn Leu Lys Thr Arg Leu Thr Pro Asn Phe Gly
50 55 60

Ile Gln Phe Tyr Thr Arg Gly Val Glu Gln Ser Leu Thr Val Gly Ala
65 70 75 80

Tyr Phe Phe Gln Asn Phe His Asn Tyr Ser Thr Asn Phe Pro Tyr Arg
85 90 95

Trp Gly Pro Thr Met Tyr Tyr Lys Ala Arg Gly Lys Arg Phe Thr Phe
100 105 110

Tyr Gly Gly Ile Phe Pro Arg Lys Asn Leu Leu Gly Arg Tyr Gly Leu
115 120 125

Asn Ile Phe Ala Pro Tyr Tyr Trp Phe Ile Asp Pro Asn Ala Arg Gly
130 135 140

Phe Leu Leu Gln Phe Gln Asn His Tyr Ser Pro Ser Lys Pro Tyr Tyr
145 150 155 160

Gly His Ala Glu Phe Met Leu Asp Trp Phe Gly Gly Asn Cys Tyr Asn
165 170 175

Thr Cys Lys Phe Gly Arg Asn Pro Tyr Gly Asn Ala Met Asp Arg Phe
180 185 190

Gln Met Asn Gly Ser Val Ala Tyr Asn Phe Phe Lys Asp Leu Leu Gly
195 200 205

Ile Gly Gly Tyr Phe Val Leu Phe His Asn Glu Asp Lys Tyr Leu Leu
210 215 220

Asn Gly Ala Asp Gly Met Gln Phe Asn Glu Lys Lys Ala Ile Asp Asn
225 230 235 240

Ser Ala Ile Tyr Leu Leu Asp Arg Leu Tyr Tyr Asn Ala Tyr Ile Ser
245 250 255

Thr Ser Leu Leu Asp Ile Ala Pro Phe Met Glu Lys Leu Ser Ala Lys
260 265 270

Phe Gly Met Val Ser Glu Ala Ser Arg Leu Arg Asn Arg Glu Lys Glu
275 280 285

Val Pro Phe Ile Asn Ser Val Gly Gly Gln Phe Asp Val Glu Ile Gln
290 295 300

Tyr Lys Gly Phe Gly Ile His Asn Leu Phe Phe Phe Ala Lys Thr Pro
305 310 315 320

Glu Met Pro Phe Tyr Asn Gln Tyr Gln Tyr Val Glu Met Tyr Cys Thr
325 330 335

Pro Ser Tyr Cys Pro Thr Pro Ile Tyr Arg Gly Val Pro Phe Phe Gln
340 345 350

Ala Asn Met Tyr Asn Arg Phe Asp Phe Tyr Tyr Asn Trp Lys Asn Asp
355 360 365

Phe Ala Ser Val Arg Ile Asn Phe Val Leu Asn Ala Met Arg Gly Gly
370 375 380

Phe Asp Arg Ser Leu Pro Trp Ser Glu Ser Tyr Gln Val Tyr Met Thr
385 390 395 400

Val Ala Phe Asp Pro Tyr Asn Leu Ile Asn Lys Ile Ala Arg Lys Lys
405 410 415

<210> 234

<211> 340

<212> PRT

<213> Helicobacter pylori

<400> 234

Met Met Ile Phe Ile Asp Ala Cys Phe Arg Lys Glu Thr Pro Tyr Thr
1 5 10 15

Pro Ile Trp Met Met Arg Gln Ala Gly Arg Tyr Leu Ser Glu Tyr Gln
20 25 30

Glu Ser Arg Lys Lys Ala Gly Ser Phe Leu Glu Leu Cys Lys Asn Ser
35 40 45

Asp Leu Ala Thr Glu Val Thr Leu Gln Pro Val Glu Ile Leu Gly Val
50 55 60

Asp Ala Ala Ile Leu Phe Ser Asp Ile Leu Val Val Pro Leu Glu Met
65 70 75 80

Gly Leu Asn Leu Glu Phe Ile Pro Lys Lys Gly Pro His Phe Leu Glu
85 90 95

Thr Ile Thr Asp Leu Lys Ser Val Glu Ser Leu Lys Val Gly Ala Tyr
100 105 110

Lys Gln Leu Asn Tyr Val Tyr Asp Thr Ile Ser Gln Thr Arg Gln Lys
115 120 125

Leu Ser Arg Glu Lys Ala Leu Ile Gly Phe Cys Gly Ser Pro Trp Thr
130 135 140

Leu Ala Thr Tyr Met Ile Glu Gly Glu Gly Ser Lys Ser Tyr Ala Lys
145 150 155 160

Ser Lys Lys Met Leu Tyr Ser Glu Pro Glu Val Leu Lys Ala Leu Leu
165 170 175

Glu Lys Leu Ser Leu Glu Leu Ile Glu Tyr Leu Ser Leu Gln Ile Gln
180 185 190

Ala Gly Val Asn Ala Val Met Ile Phe Asp Ser Trp Ala Ser Ala Leu
195 200 205

Glu Lys Glu Ala Tyr Leu Lys Phe Ser Trp Asp Tyr Leu Lys Lys Ile
210 215 220

Ser Lys Glu Leu Lys Lys Arg Tyr Ala His Ile Pro Val Ile Leu Phe
225 230 235 240

Pro Lys Gly Ile Gly Ala Tyr Leu Asp Ser Ile Asp Gly Glu Phe Asp
245 250 255

Val Phe Gly Val Asp Trp Gly Thr Pro Leu Thr Ala Ala Lys Lys Ile
260 265 270

Leu Gly Gly Lys Tyr Val Leu Gln Gly Asn Leu Glu Pro Thr Arg Leu
275 280 285

Tyr Asp Lys Asn Ala Leu Glu Glu Gly Val Glu Thr Ile Leu Lys Val
290 295 300

Met Gly Asn Gln Gly His Ile Phe Asn Leu Gly His Gly Met Leu Pro
305 310 315 320

Asp Leu Pro Arg Glu Asn Ala Lys Tyr Leu Val Gln Leu Val His Ala
325 330 335

Lys Thr Arg Arg
340

<210> 235

<211> 1028

<212> PRT

<213> Helicobacter pylori

<400> 235

Met Tyr Lys Thr Ala Ile Asn Arg Pro Ile Thr Thr Leu Met Phe Ala
1 5 10 15

Leu Ala Ile Val Phe Phe Gly Thr Met Gly Phe Lys Lys Leu Ser Val
20 25 30

Ala Leu Phe Pro Lys Ile Asp Leu Pro Thr Val Val Val Thr Thr Thr
35 40 45

Tyr Pro Gly Ala Ser Ala Glu Ile Ile Glu Ser Lys Val Thr Asp Lys
50 55 60

Ile Glu Glu Ala Val Met Gly Ile Asp Gly Ile Lys Lys Val Thr Ser
65 70 75 80

Thr Ser Ser Lys Asn Val Ser Ile Val Val Ile Glu Phe Glu Leu Glu
85 90 95

Lys Pro Asn Glu Glu Ala Leu Asn Asp Val Val Asn Lys Ile Ser Ser
100 105 110

Val Arg Phe Asp Asp Ser Asn Ile Lys Lys Pro Ser Ile Asn Lys Phe
115 120 125

Asp Thr Asp Ser Gln Ala Ile Ile Ser Leu Phe Val Ser Ser Ser Ser
130 135 140

Val Pro Ala Thr Thr Leu Asn Asp Tyr Ala Lys Asn Thr Ile Lys Pro
145 150 155 160

Met Leu Gln Lys Ile Asn Gly Val Gly Gly Val Gln Leu Asn Gly Phe
165 170 175

Arg Glu Arg Gln Ile Arg Ile Tyr Ala Asn Pro Thr Leu Met Asn Lys
180 185 190

Tyr Asn Leu Thr Tyr Ala Asp Leu Phe Ser Thr Leu Lys Ala Glu Asn
195 200 205

Val Glu Ile Asp Gly Gly Arg Ile Val Asn Ser Gln Arg Glu Phe Ser
210 215 220

Ile Leu Ile Asn Ala Asn Ser Tyr Ser Val Ala Asp Val Glu Lys Ile
225 230 235 240

Gln Val Gly Asn His Val Arg Leu Gly Asp Ile Ala Lys Ile Glu Ile
245 250 255

Gly Leu Glu Glu Asp Asn Thr Phe Ala Ser Phe Lys Asp Lys Pro Gly
260 265 270

Val Ile Leu Glu Ile Gln Lys Ile Ala Gly Ala Asn Glu Ile Glu Ile
275 280 285

Val Asp Arg Val Tyr Glu Ala Leu Lys Arg Ile Gln Ala Ile Ser Pro
290 295 300

Asn Tyr Glu Ile Arg Pro Phe Leu Asp Thr Thr Gly Tyr Ile Arg Thr
305 310 315 320

Ser Ile Glu Asp Val Lys Phe Asp Leu Val Leu Gly Ala Ile Leu Ala
325 330 335

Val Leu Val Val Phe Ala Phe Leu Arg Asn Gly Thr Ile Thr Leu Val
340 345 350

Ser Ala Ile Ser Ile Pro Ile Ser Ile Met Gly Thr Phe Ala Leu Ile
355 360 365

Gln Trp Met Gly Phe Ser Leu Asn Met Leu Thr Met Val Ala Leu Thr
370 375 380

Leu Ala Ile Gly Ile Ile Ile Asp Asp Ala Ile Val Val Ile Glu Asn
385 390 395 400

Ile His Lys Lys Leu Glu Met Gly Met Ser Lys Arg Lys Ala Ser Tyr
405 410 415

Glu Gly Val Arg Glu Ile Gly Phe Ala Leu Val Ala Ile Ser Ala Met
420 425 430

Leu Leu Ser Val Phe Val Pro Ile Gly Asn Met Lys Gly Ile Ile Gly
435 440 445

Arg Phe Phe Gln Ser Phe Gly Ile Thr Val Ala Leu Ala Ile Ala Leu
450 455 460

Ser Tyr Val Val Val Val Thr Ile Ile Pro Met Val Ser Ser Val Val
465 470 475 480

Val Asn Pro Arg His Ser Arg Phe Tyr Val Trp Ser Glu Pro Phe Phe
485 490 495

Lys Ala Leu Glu Ser Arg Tyr Thr Lys Leu Leu Gln Trp Val Leu Asn
500 505 510

His Lys Ile Ile Ile Ser Ile Ala Val Val Leu Val Phe Val Gly Ser
515 520 525

Leu Phe Val Ala Ser Lys Ile Gly Met Glu Phe Met Leu Lys Glu Asp
530 535 540

Arg Gly Arg Phe Leu Val Trp Leu Lys Ala Lys Pro Gly Val Ser Ile
545 550 555 560

Asp Tyr Met Thr Gln Lys Ser Lys Ile Phe Gln Lys Ala Ile Glu Lys
565 570 575

His Ala Glu Val Glu Phe Thr Thr Leu Gln Val Gly Tyr Gly Thr Thr
580 585 590

Gln Asn Pro Phe Lys Ala Lys Ile Phe Val Gln Leu Lys Pro Leu Lys
595 600 605

Glu Arg Lys Lys Glu His Gln Leu Gly Gln Phe Glu Leu Met Ser Val
610 615 620

Leu Arg Lys Glu Leu Arg Ser Leu Pro Glu Ala Lys Gly Leu Asp Thr
625 630 635 640

Ile Asn Leu Ser Glu Val Thr Leu Ile Gly Gly Gly Gly Asp Ser Ser
645 650 655

Pro Phe Gln Thr Phe Val Phe Ser His Ser Gln Glu Ala Val Asp Lys
660 665 670

Ser Val Glu Asn Leu Lys Lys Phe Leu Leu Glu Ser Pro Glu Leu Lys
675 680 685

Gly Lys Val Glu Ser Tyr His Thr Ser Thr Ser Glu Ser Gln Pro Gln
690 695 700

Leu Gln Leu Lys Ile Leu Arg Gln Asn Ala Asn Lys Tyr Gly Val Ser
705 710 715 720

Ala Gln Thr Ile Gly Ser Val Val Ser Ser Ala Phe Ser Gly Thr Ser
725 730 735

Gln Ala Ser Val Phe Lys Glu Asp Gly Lys Glu Tyr Asp Met Ile Ile
740 745 750

Arg Val Pro Asp Asp Lys Arg Val Ser Val Glu Asp Ile Lys Arg Leu
755 760 765

Gln Val Arg Asn Lys Tyr Asp Lys Leu Met Phe Leu Asp Ala Leu Val
770 775 780

Glu Ile Thr Glu Thr Lys Ser Pro Ser Ser Ile Ser Arg Tyr Asn Arg
785 790 795 800

Gln Arg Ser Val Thr Val Leu Ala Glu Pro Asn Arg Asn Ala Gly Val
805 810 815

Ser Leu Gly Glu Ile Leu Thr Gln Val Ser Lys Asn Thr Lys Glu Trp
820 825 830

Leu Val Glu Gly Ala Asn Tyr Arg Phe Thr Gly Glu Ala Asp Asn Ala
835 840 845

Lys Glu Ser Asn Gly Glu Phe Leu Val Ala Leu Ala Thr Ala Phe Val
850 855 860

Leu Ile Tyr Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro
865 870 875 880

Phe Ile Ile Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe
885 890 895

Ala Leu Gly Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly
900 905 910

Leu Ile Leu Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile
915 920 925

Asp Val Ala Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala
930 935 940

Ile Leu Phe Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr
945 950 955 960

Ile Ala Met Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp
965 970 975

Gly Ala Ala Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu
980 985 990

Met Ile Ser Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg
995 1000 1005

Leu Leu Ala Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn
1010 1015 1020

Gln Lys Thr Leu Glu
1025

<210> 236

<211> 194

<212> PRT

<213> Helicobacter pylori

<400> 236

Met Lys Lys Val Leu Ile Ile Asn Gly Ala Lys Ala Phe Gly Ser Ser
1 5 10 15

Gly Gly Lys Leu Asn Glu Thr Leu Thr Asp His Ala Lys Lys Thr Leu
20 25 30

Glu Ser Leu Gly Leu Glu Val Asp Thr Thr Ile Val Asp Lys Gly Tyr
35 40 45

Glu His Ala Gln Glu Val Glu Lys Val Phe Ser Ala Asp Ala Thr Ile
50 55 60

Trp Gln Met Pro Gly Trp Trp Met Gly Glu Pro Trp Ile Val Lys Lys
65 70 75 80

Tyr Ile Asp Glu Val Phe Ser Val Gly His Gly Lys Leu Tyr Ala Ser
85 90 95

Asp Gly Arg Ser Ser Gln Asn Pro Thr Lys Asn Tyr Gly Lys Gly Gly
100 105 110

Leu Met Gln Gly Lys Lys Tyr Met Leu Ser Leu Thr Trp Asn Ala Pro
115 120 125

Ile Glu Ala Phe Asn Asp Pro Ser Glu Phe Phe Glu Gly Val Gly Val
130 135 140

Asp Val Val Tyr Leu His Leu His Lys Ala Phe Gln Phe Leu Gly Leu
145 150 155 160

Ser Ala Leu Pro Thr Phe Ile Cys Asn Asp Val Val Lys Asn Pro Gln
165 170 175

Val Glu Gln Tyr Leu Asn Ser Leu Thr Thr His Leu Arg Gln Ala Phe
180 185 190

Gly Lys

<210> 237

<211> 512

<212> PRT

<213> Helicobacter pylori

<400> 237

Leu Val Phe Val Phe Leu Phe Lys Cys Val Asn Glu Glu Thr Ser Leu
1 5 10 15

Asn Phe Thr Pro Leu Leu Glu Arg Met Ala Cys Asn Leu Gln Ala Arg
20 25 30

Phe Tyr Ser Val Tyr Lys Asp Asn Thr Thr Ser Phe Tyr Leu Gln Ala
35 40 45

Ser Ala Glu Thr Thr Leu Glu Phe Ala Gln Lys Leu Ser Glu Ile Leu
50 55 60

Pro Phe Ser Leu Asp Phe Ser Phe Leu Ser Leu Lys Glu Ile Thr Glu
65 70 75 80

Pro Leu Asp Glu Asn Leu Phe Gln Thr Ala Ser Leu Ser Lys Pro Leu
85 90 95

Phe Met Asn Ala Lys Glu His Gln Asp Phe Leu Asp Lys Asn Ser Ser
100 105 110

Leu Tyr Ala Asp Thr Leu Gly Leu Ile Lys Asn Thr Ala Phe Lys Gly
115 120 125

Asp Ile Ile His Ser Pro Lys Glu Leu Ile Asp Cys Leu Thr Gln Leu
130 135 140

Lys Gly Met Leu Lys Thr Gln Asp Phe Ile Pro Ile Phe Thr Ser Arg
145 150 155 160

Glu Ala Leu Ser Leu Ser Leu Lys Asn Pro Ser Pro Ser Val Ile Phe
165 170 175

Ser Asp Leu Ser Ser Val Leu Ser Cys Thr Lys Leu Pro Leu Glu Asp
180 185 190

Ala Lys Tyr Leu Ala Ser Leu Glu Lys Pro Ser Ile Lys Ala Pro Leu
195 200 205

Lys Ser Val Phe Lys Asp Thr Phe Lys Asn Asp Glu Ile Ile Ala Gln
210 215 220

Leu Pro Tyr Asp Pro Ile Leu Asn Leu Leu Cys His Ile Leu Gln Asp
225 230 235 240

Glu Gly Ile Glu Phe Val Phe Met His Glu Ser Arg Ser Cys Glu Ala
245 250 255

Leu Leu Tyr Tyr Glu Ala Leu Phe Lys Thr Pro Lys Arg Leu Ile Thr
260 265 270

Pro Thr Lys Lys Phe Val Leu Glu Asn Asn Phe Ser Thr Phe Pro Phe
275 280 285

Lys Asp Glu Leu Glu Phe Leu Ser Ala Thr Pro Asn Ser Ile Val Leu
290 295 300

Tyr Leu Ser Phe Lys Arg Pro Thr Arg Leu Leu Leu His Ala Asn Gly
305 310 315 320

Ser Leu Lys Thr Leu Leu Ser Val Ser Phe Asp Phe Asn Lys Met Phe
325 330 335

Asn Ala Leu Lys Gln Asp Glu Lys Ala Ser Arg Met Leu Gln Asn Tyr
340 345 350

Ala Thr Lys Phe Pro Asp Phe Tyr Ala Arg Ile Val Glu Leu Ser Lys
355 360 365

Tyr Asp Leu Gly Gly Ala Asn Leu Leu Asp Phe Phe Cys Ile Leu Gly
370 375 380

Phe Val Leu Gly Tyr Ser Glu Asp Phe Cys Thr Gln Ser Val Ile Pro
385 390 395 400

Leu Ala Lys Glu Cys Leu Arg Pro Lys Gly Pro Arg Ile Asp Tyr Lys
405 410 415

Ile Leu Lys Asp Asn Ser Leu Lys Met Ala Leu Asn Phe Ser Lys Ile
420 425 430

Met His Ser Ala Met Ser Phe Arg Leu Ala Gly Val Glu Asn Glu Ile
435 440 445

Leu Ser Leu Gly Ile Leu Asp Ser Leu Ala Glu Phe Leu Gly Asn Phe
450 455 460

Ile Trp Asp Asn Ala Gln Asn Phe Ser Val Gln Glu Val Thr Ile Ala
465 470 475 480

Gly Asp Phe Phe Gly Glu Lys Val Phe Leu Asp Leu Phe Val Arg Tyr
485 490 495

Phe Pro Lys Thr Leu Ala Leu Lys Thr His Ala Phe Leu Asp Tyr Glu
500 505 510

<210> 238

<211> 916

<212> PRT

<213> Helicobacter pylori

<400> 238

Ile Lys Lys Leu Ile Leu Ser Ser Leu Val Phe Ala Cys Ile Asn Thr
1 5 10 15

Ser Val Glu Ala Leu Glu Asn Asp Gly Ser Lys Pro Asn Asp Leu Thr
20 25 30

Ser Pro Lys Glu Ala Ser Gln Glu Ser Gln Lys Asn Glu Ala Pro Lys
35 40 45

Asn Glu Val Gln Arg Asn Glu Ala Gln Lys Glu Thr Pro Gln Ser Asn
50 55 60

Gln Thr Pro Lys Glu Met Lys Val Lys Ser Ile Ser Tyr Val Gly Leu
65 70 75 80

Ser Tyr Met Ser Asp Met Leu Ala Asn Glu Ile Val Lys Ile Arg Val
85 90 95

Gly Asp Ile Val Asp Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu
100 105 110

Phe Asn Gln Gly Tyr Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly
115 120 125

Ile Leu Glu Phe His Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu
130 135 140

Ile Lys Gly Tyr Gly Thr Glu Lys Glu Lys Asp Gly Leu Lys Ser Gln
145 150 155 160

Met Gly Ile Lys Lys Gly Asp Thr Phe Asp Glu Gln Lys Leu Glu His
165 170 175

Ala Lys Thr Ala Leu Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly
180 185 190

Ser Val Val Glu Val Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu
195 200 205

Ile Val Phe Asp Val Asn Arg Gly Asp Ser Ile Tyr Ile Lys Gln Ser
210 215 220

Ile Tyr Glu Gly Ser Ala Lys Leu Lys Arg Arg Met Ile Glu Ser Leu
225 230 235 240

Ser Ala Asn Lys Gln Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn
245 250 255

Asp Gly Lys Leu Arg Leu Asp Gln Leu Glu Tyr Asp Ser Met Arg Ile
260 265 270

Gln Asp Val Tyr Met Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser
275 280 285

Pro Phe Leu Lys Thr Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr
290 295 300

Lys Val Lys Glu Gly Ile Gln Tyr Arg Ile Ser Asp Ile Leu Ile Glu
305 310 315 320

Ile Asp Asn Pro Val Val Pro Leu Lys Thr Leu Glu Lys Ala Leu Lys
325 330 335

Val Lys Arg Lys Asp Val Phe Asn Ile Glu His Leu Arg Ala Asp Ala
340 345 350

Gln Ile Leu Lys Thr Glu Ile Ala Asp Lys Gly Tyr Ala Phe Ala Val
355 360 365

Val Lys Pro Asp Leu Asp Lys Asp Glu Lys Asn Gly Leu Val Lys Val
370 375 380

Ile Tyr Arg Ile Glu Val Gly Asp Met Val Tyr Ile Asn Asp Val Ile
385 390 395 400

Ile Ser Gly Asn Gln Arg Thr Ser Asp Arg Ile Ile Arg Arg Glu Leu
405 410 415

Leu Leu Gly Pro Lys Asp Lys Tyr Asn Leu Thr Lys Leu Arg Asn Ser
420 425 430

Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile Glu
435 440 445

Glu Lys Arg Val Asn Ser Ser Leu Met Asp Leu Leu Val Ser Val Glu
450 455 460

Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser Tyr
465 470 475 480

Gly Gly Leu Met Leu Asn Gly Ser Val Ser Glu Arg Asn Leu Phe Gly
485 490 495

Thr Gly Gln Ser Met Ser Leu Tyr Ala Asn Ile Ala Thr Gly Gly Gly
500 505 510

Arg Ser Tyr Pro Gly Met Pro Lys Gly Ala Gly Arg Met Phe Ala Gly
515 520 525

Asn Leu Ser Leu Thr Asn Pro Arg Ile Phe Asp Ser Trp Tyr Ser Ser
530 535 540

Thr Ile Asn Leu Tyr Ala Asp Tyr Arg Ile Ser Tyr Gln Tyr Ile Gln
545 550 555 560

Gln Gly Gly Gly Phe Gly Val Asn Val Gly Arg Met Leu Gly Asn Arg
565 570 575

Thr His Val Ser Leu Gly Tyr Asn Leu Asn Val Thr Lys Leu Leu Gly
580 585 590

Phe Ser Ser Pro Leu Tyr Asn Arg Tyr Tyr Ser Ser Val Asn Glu Val
595 600 605

Val Ser Pro Arg Gln Cys Ser Thr Pro Ala Ser Val Ile Ile Asn Arg
610 615 620

Leu Ser Gly Gly Lys Thr Pro Leu Gln Pro Glu Ser Cys Ser Ser Pro
625 630 635 640

Gly Ala Ile Thr Thr Ser Pro Glu Ile Arg Gly Ile Trp Asp Arg Asp
645 650 655

Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp Val Ser Tyr Asp
660 665 670

Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val Ile Phe Ser Ser
675 680 685

Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr Leu Asn Ser Trp
690 695 700

Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly Lys Phe
705 710 715 720

Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu Ile Ala
725 730 735

Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr Asp Asp
740 745 750

Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr Thr Val
755 760 765

Arg Gly Phe Arg Asn Gly Ser Val Thr Pro Lys Asp Glu Phe Gly Leu
770 775 780

Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr Glu Leu Ser Tyr
785 790 795 800

Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe Asp Phe
805 810 815

Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr Asn
820 825 830

Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly Ala
835 840 845

Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile Glu
850 855 860

Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala Phe
865 870 875 880

Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu Cys
885 890 895

Phe Asn Pro Asn Met Asp Asp Tyr Thr Gln His Phe Glu Phe Ser Met
900 905 910

Gly Thr Arg Phe
915

<210> 239

<211> 414

<212> PRT

<213> Helicobacter pylori

<400> 239

Met Arg Lys Ile Phe Ser Tyr Val Leu Lys Ala Leu Leu Phe Ile Gly
1 5 10 15

Ile Val Tyr Ala Glu Pro Glu Ser Lys Val Glu Ala Leu Glu Gly Arg
20 25 30

Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys Asn
35 40 45

Lys Asp Leu Lys Asn Lys Glu Leu Lys Asn Lys Lys Glu Glu Lys Lys
50 55 60

Asn Thr Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala
65 70 75 80

Glu Val His His Gly Asp Thr Lys Asn Pro Thr Gln Lys Ile Thr Pro
85 90 95

Pro Lys Ile Lys Glu Asn Ala Lys Gly Val Gln Asn Gln Gly Val Gln
100 105 110

Ser Asn Ala Pro Lys Leu Glu Glu Lys Asp Thr Thr Ser Gln Thr Leu
115 120 125

Glu Lys Lys Gly Ala Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly
130 135 140

Asn Pro Asn Asp Ala Ala Asn Asn Thr Leu Glu Asp Lys Val Val Gly
145 150 155 160

Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
165 170 175

Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Lys Ala Gln Ala Arg Asp
180 185 190

Arg Leu Ile Ala Glu Arg Ile Lys Asn Gln Glu Ile Glu Arg Leu Lys
195 200 205

Ile His Val Asp Asp Asp Lys Leu Asp Gln Glu Met Ala Met Met Ala
210 215 220

Gln Gln Gln Gly Met Asp Leu Asp His Phe Lys Gln Met Leu Met Ala
225 230 235 240

Glu Gly His Tyr Lys Leu Tyr Arg Asp Gln Leu Lys Glu His Leu Glu
245 250 255

Met Gln Glu Leu Leu Arg Asn Ile Leu Leu Thr Asn Val Asp Thr Ser
260 265 270

Ser Glu Thr Lys Met Arg Glu Tyr Tyr Asn Lys His Lys Glu Gln Phe
275 280 285

Ser Ile Pro Thr Glu Ile Glu Thr Val Arg Tyr Thr Ser Thr Asn Gln
290 295 300

Glu Asp Leu Glu Arg Ala Met Ala Asp Pro Asn Leu Glu Ile Pro Gly
305 310 315 320

Val Ser Lys Ala Asn Glu Lys Ile Glu Met Lys Thr Leu Asn Pro Gln
325 330 335

Ile Ala Gln Val Phe Ile Ser His Glu Gln Gly Ser Phe Thr Pro Val
340 345 350

Met Asn Gly Gly Gly Gly Gln Phe Ile Thr Phe Tyr Ile Lys Glu Lys
355 360 365

Lys Gly Lys Asn Glu Val Ser Phe Ser Gln Ala Lys Gln Phe Ile Ala
370 375 380

Gln Lys Leu Val Glu Glu Ser Lys Asp Lys Ile Leu Glu Glu His Phe
385 390 395 400

Glu Lys Leu Arg Val Lys Ser Arg Ile Val Met Ile Arg Glu
405 410

<210> 240

<211> 433

<212> PRT

<213> Helicobacter pylori

<400> 240

Met Leu Ser Val Ile Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg
1 5 10 15

Ser Ser Leu Pro Lys Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu
20 25 30

Phe Tyr Ile Leu Glu Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu
35 40 45

Ile Leu His His Gln Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg
50 55 60

Phe Lys Gly Val Ile Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly
65 70 75 80

Thr Gly Gly Ala Ile Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys
85 90 95

His Glu Arg Val Leu Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys
100 105 110

Asp Ala Leu Ala Pro Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu
115 120 125

Leu His Leu Ala Asp Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn
130 135 140

His Gln Val Lys Lys Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu
145 150 155 160

Lys Glu Ile Lys Ser Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp
165 170 175

Phe Leu Glu Lys Tyr Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys
180 185 190

Glu Tyr Tyr Leu Thr Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu
195 200 205

Thr Ile Asp Ala Ile Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn
210 215 220

Ser Gln Thr Glu Arg Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu
225 230 235 240

Arg Lys Asn Ala Met Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser
245 250 255

Ile Tyr Leu Glu Lys Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu
260 265 270

Gln Gly Val Arg Leu Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile
275 280 285

Lys Ala Tyr Ser Val Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val
290 295 300

Gly Pro Phe Ala His Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His
305 310 315 320

Val Gly Asn Phe Val Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys
325 330 335

Ala Gly His Leu Ser Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr
340 345 350

Asn Val Gly Ala Gly Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys
355 360 365

His Gln Thr Ile Ile Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln
370 375 380

Leu Val Ala Pro Ile Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly
385 390 395 400

Thr Thr Ile Thr Lys Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg
405 410 415

Ala Pro Gln Thr Asn Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys
420 425 430

Pro

<210> 241

<211> 642

<212> PRT

<213> Helicobacter pylori

<400> 241

Met Lys Glu Ile Thr Ile Ala Leu Val Gly Gln Pro Asn Val Gly Lys
1   5   10   15

Ser Ser Leu Ile Asn Ala Leu Ser Asn Ala His Leu Lys Val Gly Asn
            20   25   30

Phe Ala Gly Val Thr Val Asp Lys Met Glu Val Gly Leu Ile His Lys
        35   40   45

Glu His Gln Ile Thr Ile Ile Asp Leu Pro Gly Thr Tyr Ala Leu Asn
    50   55   60

Asp Phe Thr Thr Glu Glu Lys Val Thr Lys Asp Phe Leu Glu Lys Gly
65   70   75   80

Gln Tyr Asp Leu Ile Leu Asn Val Val Asp Ser Thr Asn Leu Glu Arg
                85   90   95

Asn Leu Ala Leu Ser Ala Gln Leu Leu Asp Thr Asn Lys Lys Met Leu
            100   105   110

Leu Ala Leu Asn Met Trp Asp Glu Ala Gln Lys Glu Gly Ile Lys Ile
        115   120   125

Asn Thr Glu Lys Leu Ser Lys Glu Leu Gly Val Val Cys Val Pro Thr
    130   135   140

Ser Ala Arg Ser Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp
145   150   155   160

Glu Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile
                165   170   175

Lys Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser
            180   185   190

Ala Gln Arg Ile Ala Gln Leu Val Ile Ser Glu Asn Gln Gln Asn Ala
        195   200   205

Ser Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Leu Met His Lys Arg
    210   215   220

Tyr Gly Ile Phe Ile Phe Leu Gly Phe Met Phe Ile Ile Phe Ser Leu
225   230   235   240

Ser Phe Leu Ile Gly Gly Gly Val Gln Lys Ala Leu Glu Thr Gly Phe
                245   250   255

Lys Phe Leu Ser Asp Gly Ile Lys Glu Asn Val Ala Asn Glu Asp Leu
            260   265   270

Ala Ser Leu Val Gly Asp Gly Ile Ile Gly Gly Val Gly Ala Thr Val
275 280 285

Ser Phe Leu Pro Leu Ile Val Val Leu Tyr Phe Gly Ile Ser Leu Leu
290 295 300

Glu Thr Thr Gly Tyr Met Ser Arg Val Ala Phe Leu Leu Asp Gly Ile
305 310 315 320

Leu His Lys Phe Gly Leu His Gly Lys Ser Phe Ile Pro Leu Ile Thr
325 330 335

Gly Phe Gly Cys Ser Val Pro Ala Tyr Met Ala Thr Arg Thr Leu Gln
340 345 350

Asn Tyr Asn Glu Arg Leu Ile Thr Leu Phe Val Ile Gly Phe Met Ser
355 360 365

Cys Ser Ala Arg Leu Pro Ile Tyr Val Leu Phe Val Gly Ser Phe Phe
370 375 380

Pro Ser Ser Ser Ala Gly Phe Val Leu Phe Cys Ile Tyr Ile Leu Gly
385 390 395 400

Ala Val Val Ala Leu Val Met Ala Lys Leu Leu Lys Leu Ser Val Phe
405 410 415

Lys Gly Gln Thr Glu Ser Phe Ile Met Glu Met Pro Lys Tyr Arg Phe
420 425 430

Pro Ser Trp Arg Met Val Tyr Phe Ser Ile Tyr Thr Lys Ser Leu Ser
435 440 445

Tyr Leu Lys Lys Ala Gly Thr Tyr Ile Leu Val Gly Ala Ile Leu Ile
450 455 460

Trp Phe Met Ser Gln Tyr Pro Lys Ser Asp Ala Ala Met Lys Ala Tyr
465 470 475 480

Lys Gln Glu Ser Leu Leu Val Asn Lys Asp Thr Thr Leu Ser Ser Glu
485 490 495

Ala Lys Glu Glu Lys Leu Lys Glu Leu Lys Thr Glu Leu Asp Lys Lys
500 505 510

Asn Leu Lys Asn Ser Ile Val Gly Arg Gly Gly Ala Tyr Leu Glu Lys
515 520 525

Val Phe Ser Pro Met Asp Phe Asp Trp Arg Leu Ser Val Ser Leu Val
530 535 540

Thr Gly Phe Met Ala Lys Glu Val Val Val Ser Thr Leu Gly Val Leu
545 550 555 560

Phe Ser Leu Gly Asp Gln Asn Glu Lys Ser Asp Ala Phe Arg Gly Ile
565 570 575

Leu Arg Lys Glu Val Ser Val Pro Ser Gly Ile Ala Phe Ile Val Phe
580 585 590

Val Met Phe Tyr Ile Pro Cys Phe Ala Ala Thr Ile Thr Phe Gly Arg
595 600 605

Glu Ala Gly Gly Ile Lys Phe Val Ala Tyr Leu Phe Ile Phe Thr Thr
610 615 620

Val Val Ala Tyr Ala Phe Ser Leu Ile Ala Phe Tyr Ala Thr Gln Ile
625 630 635 640

Leu Val

<210> 242

<211> 765

<212> PRT

<213> Helicobacter pylori

<400> 242

Met Ala Asn Leu Leu Lys Asn Gly Lys Thr Leu Lys Gln Ala Arg Asp
1 5 10 15

Glu Ile Leu Ala Arg Thr Glu Lys Thr Gly His Tyr Asn Gly Leu Lys
20 25 30

Lys Leu Glu Phe Lys Glu Arg Asp Pro Ile Gly Tyr Glu Lys Met Phe
35 40 45

Ser Lys Leu Arg Gly Gly Ile Val His Ala Arg Glu Thr Ala Lys Arg
50 55 60

Ile Ala Ala Ser Pro Ile Val Glu Gln Glu Gly Glu Leu Cys Phe Thr
65 70 75 80

Leu Tyr Asn Ala Val Gly Asp Ser Val Leu Thr Ser Thr Gly Ile Ile
85 90 95

Ile His Val Gly Thr Met Gly Ser Ala Ile Lys Tyr Met Val Glu Asn
100 105 110

Asn Trp Glu Asp Asn Pro Gly Ile Asn Asp Lys Asp Ile Phe Thr Asn
115 120 125

Asn Asp Cys Ala Ile Gly Asn Val His Pro Cys Asp Ile Met Thr Leu
130 135 140

Val Pro Ile Phe His Asp Glu Lys Leu Ile Gly Trp Val Gly Gly Val
145 150 155 160

Thr His Val Ile Asp Thr Gly Ser Val Thr Pro Gly Ser Met Ser Thr
165 170 175

Gly Gln Val Gln Arg Phe Gly Asp Gly Tyr Met Ile Thr Cys Arg Lys
180 185 190

Thr Gly Ala Asn Asp Glu Ser Phe Lys Asp Trp Leu His Glu Ser Gln
195 200 205

Arg Ser Val Arg Thr Pro Lys Tyr Trp Ile Leu Asp Glu Arg Thr Arg
210 215 220

Ile Ala Gly Cys His Met Ile Arg Asp Leu Val Met Glu Val Ile Lys
225 230 235 240

Glu Asp Gly Ile Asp Ser Tyr Met Arg Phe Ile Asp Glu Val Ile Glu
245 250 255

Glu Gly Arg Arg Gly Leu Ile Ser Arg Ile Lys Ser Met Thr Ile Pro
260 265 270

Gly Lys Tyr Arg Lys Val Ala Phe Val Asp Val Pro Tyr Ala His Lys
275 280 285

Asp Ile Gly Val Cys Ser Glu Phe Ala Lys Leu Asp Thr Ile Met His
290 295 300

Ser Pro Val Glu Ile Thr Ile Asn Lys Asp Ala Thr Trp Lys Leu Asp
305 310 315 320

Phe Asp Gly Ala Ser Arg Trp Gly Trp His Ser Phe Asn Cys Asn Gln
325 330 335

Val Ser Phe Thr Ser Gly Ile Trp Val Met Met Thr Gln Thr Leu Ile
340 345 350

Pro Thr Ser Arg Ile Asn Asp Gly Ala Tyr Phe Ala Thr Gln Phe Arg
355 360 365

Leu Lys Lys Gly Thr Trp Met Asn Pro Asp Asp Arg Arg Thr Gly His
370 375 380

Ala Tyr Ala Trp His Phe Leu Val Ser Gly Trp Ser Ala Leu Trp Arg
385 390 395 400

Gly Leu Ser Gln Ala Tyr Tyr Ser Arg Gly Tyr Leu Glu Glu Val Asn
405 410 415

Ser Gly Asn Ala Asn Thr Ser Asn Trp Leu Gln Gly Gly Gly Ile Asn
420 425 430

Gln Asp Gly Glu Ile His Ala Val Asn Ser Phe Glu Thr Ser Ser Cys
435 440 445

Gly Thr Gly Ala Cys Ala Ile Lys Asp Gly Leu Asn His Ala Ala Ala
450 455 460

Ile Trp Asn Pro Glu Gly Asp Met Gly Asp Val Glu Ile Trp Glu Met
465 470 475 480

Ala Glu Pro Leu Leu Tyr Leu Gly Arg Asn Val Lys Ala Asn Thr Gly
485 490 495

Gly Tyr Gly Lys Tyr Arg Gly Gly Asn Gly Phe Glu Thr Leu Arg Met
500 505 510

Val Trp Gly Ala His Asp Trp Thr Met Phe Phe Met Gly Asn Gly Tyr
515 520 525

Met Asn Ser Asp Trp Gly Met Met Gly Gly Tyr Pro Ala Ala Ser Gly
530 535 540

Tyr Arg Phe Glu Ala His Asn Thr Asp Leu Lys Asn Arg Ile Lys Asn
545 550 555 560

Asn Ala Ser Leu Pro Leu Gly Gly Asp Phe Asn Pro Thr Asp Arg Asp
565 570 575

Tyr Glu Lys His Ile Ser His Ala Ser Gln Val Lys Arg Asp Lys Gln
580 585 590

Cys Ile Thr Thr Glu Asn Cys Phe Asp Asn Tyr Asp Leu Tyr Leu Asn
595 600 605

Tyr Ile Lys Gly Gly Pro Gly Phe Gly Asp Pro Ile Glu Arg Asp Leu
610 615 620

Asn Ala Ile Leu Glu Asp Leu Asn Ser Lys Gln Leu Leu Pro Glu Tyr
625 630 635 640

Ala Tyr Lys Val Tyr Gly Ala Val Val Ser Gln Asn Lys Asp Gly Val
645 650 655

Trp Val Gly Asp Glu Ala Lys Thr Lys Ala Arg Arg Lys Glu Ile Leu
660 665 670

Glu Asn Arg Lys Ala Arg Ser Ile Pro Val Lys Gln Trp Met Glu Gln
675 680 685

Glu Arg Asn Ala Ile Leu Glu Lys Glu Ala Ser Lys Gln Val Lys His
690 695 700

Met Tyr Ala Thr Ser Phe Asp Leu Ser Pro Lys Phe Leu Asn Asp Phe
705 710 715 720

Lys Thr Phe Trp Asn Leu Pro Lys Asn Trp Ser Val Lys Glu Asp Glu
725 730 735

Leu Gly Val Phe Thr Tyr Gly Ser Lys Tyr Arg Met Asp Leu Ser Lys
740 745 750

Leu Pro Asp Val Arg Thr Val Leu Leu Val Asp Glu Lys
755 760 765

<210> 243

<211> 827

<212> PRT

<213> Helicobacter pylori

<400> 243

Met Gln Asp Asn Ser Val Asn Glu Thr Lys Asn Ile Val Glu Val Gly
1 5 10 15

Ile Asp Ser Ser Ile Glu Glu Ser Tyr Leu Ala Tyr Ser Met Ser Val
20 25 30

Ile Ile Gly Arg Ala Leu Pro Asp Ala Arg Asp Gly Leu Lys Pro Val
35 40 45

His Arg Arg Ile Leu Tyr Ala Met His Glu Leu Gly Leu Thr Ser Lys
50 55 60

Val Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys
65 70 75 80

Tyr His Pro His Gly Asp Asn Ala Val Tyr Asp Ala Leu Val Arg Met
85 90 95

Ala Gln Asp Phe Ser Met Arg Leu Glu Leu Val Asp Gly Gln Gly Asn
100 105 110

Phe Gly Ser Ile Asp Gly Asp Asn Ala Ala Ala Met Arg Tyr Thr Glu
115 120 125

Ala Arg Met Thr Lys Ala Ser Glu Glu Ile Leu Arg Asp Ile Asp Lys
130 135 140

Asp Thr Ile Asp Phe Val Pro Asn Tyr Asp Asp Thr Leu Lys Glu Pro
145 150 155 160

Asp Ile Leu Pro Ser Arg Leu Pro Asn Leu Leu Val Asn Gly Ala Asn
165 170 175

Gly Ile Ala Val Gly Met Ala Thr Ser Ile Pro Pro His Arg Met Asp
180 185 190

Glu Ile Ile Asp Ala Leu Val His Val Leu Glu Asn Pro Asn Ala Gly
195 200 205

Leu Asp Glu Ile Leu Glu Phe Val Lys Gly Pro Asp Phe Pro Thr Gly
210 215 220

Gly Ile Ile Tyr Gly Lys Ala Gly Ile Ile Glu Ala Tyr Lys Thr Gly
225 230 235 240

Arg Gly Arg Val Lys Val Arg Ala Lys Val His Val Glu Lys Thr Lys
245 250 255

Asn Lys Glu Ile Ile Val Leu Asp Glu Met Pro Phe Gln Thr Asn Lys
260 265 270

Ala Lys Leu Val Glu Gln Ile Ser Asp Leu Ala Arg Glu Lys Gln Ile
275 280 285

Glu Gly Ile Ser Glu Val Arg Asp Glu Ser Asp Arg Glu Gly Ile Arg
290 295 300

Val Val Ile Glu Leu Lys Arg Asp Ala Met Ser Glu Ile Val Leu Asn
305 310 315 320

His Leu Tyr Lys Leu Thr Thr Met Glu Thr Thr Phe Ser Ile Ile Leu
325 330 335

Leu Ala Ile Tyr Asn Lys Glu Pro Lys Ile Phe Thr Leu Leu Glu Leu
340 345 350

Leu His Leu Phe Leu Asn His Arg Lys Thr Ile Ile Ile Arg Arg Thr
355 360 365

Ile Phe Glu Leu Glu Lys Ala Lys Ala Arg Ala His Ile Leu Glu Gly
370 375 380

Tyr Leu Ile Ala Leu Asp Asn Ile Asp Glu Ile Val Arg Leu Ile Lys
385 390 395 400

Thr Ser Gln Ser Pro Glu Ala Ala Lys Asn Ala Leu Met Glu Arg Phe
405 410 415

Thr Leu Ser Glu Ile Gln Ser Lys Ala Ile Leu Glu Met Arg Leu Gln
420 425 430

Arg Leu Thr Gly Leu Glu Arg Asp Lys Ile Lys Glu Glu Tyr Gln Asn
435 440 445

Leu Leu Glu Leu Ile Asp Asp Leu Asn Gly Ile Leu Lys Ser Glu Asp
450 455 460

Arg Leu Asn Gly Val Val Lys Thr Glu Leu Leu Glu Val Lys Glu Gln
465 470 475 480

Phe Ser Ser Pro Arg Arg Thr Glu Ile Gln Glu Ser Tyr Glu Asn Ile
485 490 495

Asp Ile Glu Asp Leu Ile Ala Asn Glu Pro Met Val Val Ser Met Ser
500 505 510

Tyr Lys Gly Tyr Val Lys Arg Val Asp Leu Lys Ala Tyr Glu Lys Gln
515 520 525

Asn Arg Gly Gly Lys Gly Lys Leu Ser Gly Ser Thr Tyr Glu Asp Asp
530 535 540

Phe Ile Glu Asn Phe Phe Val Ala Asn Thr His Asp Ile Leu Leu Phe
545 550 555 560

Ile Thr Asn Lys Gly Gln Leu Tyr His Leu Lys Val Tyr Lys Ile Pro
565 570 575

Glu Ala Ser Arg Ile Ala Met Gly Lys Ala Ile Val Asn Leu Ile Ser
580 585 590

Leu Ala Pro Asp Glu Lys Ile Met Ala Thr Leu Ser Thr Lys Asp Phe
595 600 605

Ser Asp Glu Arg Ser Leu Ala Phe Phe Thr Lys Asn Gly Val Val Lys
610 615 620

Arg Thr Asn Leu Ser Glu Phe Glu Ser Asn Arg Ser Cys Gly Ile Arg
625 630 635 640

Ala Ile Val Leu Asp Glu Gly Asp Glu Leu Val Ser Ala Lys Val Val
645 650 655

Asp Lys Asn Ala Lys His Leu Leu Ile Ala Ser His Leu Gly Ile Phe
660 665 670

Ile Lys Phe Pro Leu Glu Glu Val Arg Glu Ile Gly Arg Thr Thr Arg
675 680 685

Gly Val Ile Gly Ile Lys Leu Asn Glu Asn Asp Phe Val Val Gly Ala
690 695 700

Val Val Ile Ser Asp Asp Gly Asn Lys Leu Leu Ser Val Ser Glu Asn
705 710 715 720

Gly Leu Gly Lys Gln Thr Leu Ala Glu Ala Tyr Arg Gly Gln Ser Arg
725 730 735

Gly Gly Lys Gly Val Ile Gly Met Lys Leu Thr Gln Lys Thr Gly Asn
740 745 750

Leu Val Gly Val Ile Ser Val Asp Asp Glu Asn Leu Asp Leu Met Ile
755 760 765

Leu Thr Ala Ser Ala Lys Met Ile Arg Val Ser Ile Lys Asp Ile Arg
770 775 780

Glu Thr Gly Arg Asn Ala Ser Gly Val Lys Leu Ile Asn Thr Ala Asp
785 790 795 800

Lys Val Met Tyr Val Asn Ser Cys Pro Lys Glu Glu Glu Pro Glu Asn
805 810 815

Leu Glu Thr Ser Ser Ala Gln Asn Leu Phe Glu
820 825

<210> 244

<211> 273

<212> PRT

<213> Helicobacter pylori

<400> 244

Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1 5 10 15

Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
20 25 30

Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
35 40 45

Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
50 55 60

Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ala Lys Tyr
65 70 75 80

Ala Asn Gly Ala Leu Asn Gly Leu Gly Leu Asn Val Gly Tyr Lys Lys
85 90 95

Phe Phe Gln Phe Lys Ser Phe Asp Met Thr Ser Lys Trp Phe Gly Phe
100 105 110

Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Thr Leu Gly Lys Gln
115 120 125

Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
130 135 140

Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Asn Asp Asn Ala Ser Phe
145 150 155 160

Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
165 170 175

Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp
180 185 190

Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Lys
195 200 205

Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
210 215 220

Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu
225 230 235 240

Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
245 250 255

Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
260 265 270

Phe

<210> 245

<211> 414

<212> PRT

<213> Helicobacter pylori

<400> 245

Met Ala Ile Leu Arg Ala Asn Leu Ser Pro Lys Asn Lys Leu Asn Ala
1   5   10   15

Thr Leu Lys Gly Trp Leu Pro Ile Leu Gln Ser Glu Leu Glu Asp Leu
            20   25   30

Glu Glu Val Leu Lys Gln Asn Ala Leu Asp Asn Pro Leu Ile Lys Ile
        35   40   45

Glu Asn Lys Arg Ile Lys Asn Phe Ser Asp Arg Phe Ser Ala Lys Lys
    50   55   60

Ser Ser Asp His Leu Glu Asn Phe Ala Thr Ala Ser Lys Ser Leu Phe
65   70   75   80

Glu Thr Leu Glu Ala Gln Ile Ile Pro Pro Leu Phe Pro Thr Glu Thr
                85   90   95

Ser Gln Lys Ile Ala Met Asp Ile Ile Ser Gly Leu Asn Asn Glu Gly
            100   105   110

Tyr Phe Glu Glu Asn Ile Glu Glu Arg Ala Arg Ile Leu Gly Val Glu
        115   120   125

Ser Glu Val Tyr Glu Lys Val Arg Lys Arg Phe Ser Tyr Leu Asn Pro
    130   135   140

Ala Gly Ile Gly Ala Lys Asp Val Lys Glu Ser Phe Leu Phe Gln Leu
145   150   155   160

Glu Ser Arg Glu Leu Asp Asp Asn Glu Leu Tyr Glu Glu Thr Arg Lys
                165   170   175

Ile Ile Leu Asn Leu Glu Lys His His Glu Phe Ser Lys Asp Phe Tyr
            180   185   190

Tyr Glu Lys Ala Leu Lys Ile Leu Lys Ser Phe Lys Asn Pro Pro Ala
        195   200   205

Ile Glu Phe Leu Glu Lys Glu Ile Glu Val Ile Pro Glu Leu Phe Ile
    210   215   220

Val Glu Val Asp Asn Gly Ile Ile Val Arg Leu Asn Asp Glu Ser Tyr
225   230   235   240

Pro Thr Ile Ser Leu Glu Glu Asn Arg Phe Lys Asp Ser Gly Tyr Leu
                245   250   255

Lys Glu Lys Leu Lys Glu Ala Lys Asp Leu Ile Asp Ala Leu Asn Leu
260 265 270

Arg Lys Ala Thr Ile Tyr Lys Ile Gly Leu Met Leu Leu Glu Tyr Gln
275 280 285

Tyr Asp Phe Phe Lys Gly Lys Glu Leu Arg Pro Leu Lys Leu Leu Asp
290 295 300

Leu Ala Asn Glu Phe Asn His Ser Val Ser Thr Ile Ser Arg Ala Ile
305 310 315 320

Ser Asn Lys Tyr Leu Ala Cys Glu Arg Gly Val Phe Pro Ile Lys His
325 330 335

Phe Phe Ser Ile Ala Leu Asp Asn Ser Glu Thr Ser Asn Ala Val Ile
340 345 350

Lys Asp Tyr Leu Leu Glu Leu Ile Lys Asn Glu Asp Lys Lys Glu Pro
355 360 365

Leu Ser Asp Ala Lys Ile Leu Glu Leu Ile Glu Glu Lys Phe His Leu
370 375 380

Lys Met Val Arg Arg Thr Ile Thr Lys Tyr Arg Gln Leu Leu Asn Ile
385 390 395 400

Ala Ser Ser Ser Glu Arg Lys Arg Leu Tyr Leu Met Arg Ala
405 410

<210> 246

<211> 578

<212> PRT

<213> Helicobacter pylori

<400> 246

Met Gln Val Leu Ala Leu Lys Tyr Arg Pro Lys His Phe Ser Glu Leu
1 5 10 15

Val Gly Gln Glu Ser Val Ala Lys Thr Leu Ser Leu Ala Leu Asp Asn
20 25 30

Gln Arg Leu Ala Asn Ala Tyr Leu Phe Ser Gly Leu Arg Gly Ser Gly
35 40 45

Lys Thr Ser Ser Ser Arg Ile Phe Ala Arg Ala Leu Met Cys Glu Glu
50 55 60

Gly Pro Lys Ala Val Pro Cys Asp Thr Cys Ile Gln Cys Gln Ser Ala
65 70 75 80

Leu Asn Asn His His Ile Asp Ile Ile Glu Met Asp Gly Ala Ser Asn
85 90 95

Arg Gly Ile Asp Asp Val Arg Asn Leu Ile Glu Gln Thr Arg Tyr Lys
100 105 110

Pro Ser Phe Gly Arg Tyr Lys Ile Phe Ile Ile Asp Glu Val His Met
115 120 125

Phe Thr Thr Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
130 135 140

Pro Ser His Val Lys Phe Leu Leu Ala Thr Thr Asp Ala Leu Lys Leu
145 150 155 160

Pro Ala Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Lys Lys Ile
165 170 175

Pro Glu Asn Ser Val Ile Ser His Leu Lys Thr Ile Leu Glu Lys Glu
180 185 190

Gln Val Ser Tyr Glu Thr Ser Ala Leu Glu Lys Leu Ala His Ser Gly
195 200 205

Gln Gly Ser Leu Arg Asp Thr Ile Thr Leu Leu Glu Gln Ala Ile Asn
210 215 220

Tyr Cys Asp Asn Ala Ile Thr Glu Ser Lys Val Ala Glu Met Leu Gly
225 230 235 240

Ala Ile Asp Arg Ser Val Leu Glu Asp Phe Phe Gln Ser Leu Ile Asn
245 250 255

Gln Asp Glu Ala Arg Leu Lys Glu Arg Tyr Ala Ile Leu Glu Asn Tyr
260 265 270

Glu Thr Glu Ser Val Leu Glu Glu Met Met Leu Phe Leu Lys Ala Lys
275 280 285

Leu Leu Ser Pro Asp Phe Tyr Ser Ile Leu Leu Ile Glu Arg Phe Phe
290 295 300

Lys Ile Ile Met Ser Ser Leu Ser Leu Leu Lys Glu Gly Ala Asn Ala
305 310 315 320

Ser Phe Val Leu Leu Leu Leu Lys Met Lys Phe Lys Glu Ala Leu Lys
325 330 335

Phe Lys Ala Leu Asp Asp Ala Ile Leu Glu Leu Glu Gln Thr Pro Phe
340 345 350

Asn Gln Asn Pro Ser Ile Ser Tyr Asn Ala Pro Lys Gln Glu Ser Lys
355 360 365

Asn Ile Glu Lys Arg Glu Lys Ile Glu Gln Ile Glu Arg Ile Glu Gly
370 375 380

Thr Glu Lys Arg Glu Lys Leu Glu Lys Lys Glu Asn Ala Glu Thr Pro
385 390 395 400

Gln Thr Pro Met Leu Ser Ala Lys Asp Arg Ile Phe His Asn Leu Phe
405 410 415

Lys Gln Val Gln Thr Leu Val Tyr Glu Arg Asn Tyr Glu Leu Gly Ala
420 425 430

Val Phe Glu Lys Asn Ile Arg Phe Ile Asp Phe Asp Ser Gln Thr Lys
435 440 445

Thr Leu Thr Trp Glu Ser Leu Ala Thr Asp Lys Asp Lys Glu Leu Leu
450 455 460

Arg Glu Arg Phe Lys Ile Val Lys Ser Ile Val Asp Gly Val Phe Gly
465 470 475 480

Lys Gly Glu Ser Ile Lys Ile Ala Leu Lys Asn His Ser Glu Asn Lys
485 490 495

Ser Thr Leu Glu Val Val Lys Glu Leu Lys Phe Pro Tyr Ser Lys Pro
500 505 510

Lys Pro Thr Thr Glu Thr Thr Ala Glu Thr Lys Glu Lys Glu Thr Lys
515 520 525

Glu Lys Glu Ile Gln Glu Asn Asp Thr Lys Glu Ile Gln Glu Val Gln
530 535 540

Pro Lys Gln Ala Pro Thr Ala Leu Gln Glu Phe Met Ala Asn His Ser
545 550 555 560

Glu Leu Ile Glu Glu Ile Lys Ser Glu Phe Glu Ile Lys Ser Val Glu
565 570 575

Leu Leu

<210> 247

<211> 348

<212> PRT

<213> Helicobacter pylori

<400> 247

Met Arg Ile Phe Leu Lys Leu Leu Ile Leu Leu Phe Cys Leu Lys Gly
1 5 10 15

Gln Val Met Ala Gln Asn Leu Pro Thr Ile Ala Leu Leu Ala Thr Gly
20 25 30

Gly Thr Ile Ala Gly Ser Gly Ala Ser Ala Ser Leu Gly Ser Tyr Lys
35 40 45

Ser Gly Glu Leu Gly Ile Lys Glu Leu Leu Lys Ala Ile Pro Ser Leu
50 55 60

Asn Arg Leu Ala Arg Ile Gln Gly Glu Gln Ile Ser Asn Ile Gly Ser
65 70 75 80

Gln Asp Met Asn Glu Glu Val Trp Phe Lys Leu Ala Lys Arg Ala Gln
85 90 95

Glu Leu Leu Asp Asp Ser Arg Ile Gln Gly Val Val Ile Thr His Gly
100 105 110

Thr Asp Thr Leu Glu Glu Ser Ala Tyr Phe Leu Asn Leu Val Leu Arg
115 120 125

Ser Thr Lys Pro Val Val Leu Val Gly Ala Met Arg Asn Ala Ala Ser
130 135 140

Leu Ser Ala Asp Gly Ala Leu Asn Leu Tyr Asn Ala Val Ser Val Ala
145 150 155 160

Leu Asn Glu Lys Ser Ala Asn Lys Gly Val Leu Val Val Met Asp Asp
165 170 175

Asn Ile Phe Ser Ala Arg Glu Val Ile Lys Thr His Thr Thr His Thr
180 185 190

Ser Thr Phe Lys Ala Leu Asn Ser Gly Ala Ile Gly Ser Val Tyr Tyr
195 200 205

Gly Lys Thr Arg Tyr Tyr Met Gln Pro Leu Arg Lys His Thr Thr Glu
210 215 220

Ser Glu Phe Ser Leu Ser Gln Leu Lys Thr Pro Leu Pro Lys Val Asp
225 230 235 240

Ile Ile Tyr Thr His Ala Gly Met Thr Pro Asp Leu Phe Gln Ala Ser
245 250 255

Leu Asn Ser His Ala Lys Gly Val Val Ile Ala Gly Val Gly Asn Gly
260 265 270

Asn Val Ser Ala Gly Phe Leu Lys Ala Met Gln Glu Ala Ser Gln Met
275 280 285

Gly Val Val Ile Val Arg Ser Ser Arg Val Asn Ser Gly Glu Ile Thr
290 295 300

Ser Gly Glu Ile Asp Asp Lys Ala Phe Ile Thr Ser Asp Asn Leu Asn
305 310 315 320

Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Lys Thr Asn
325 330 335

Asn Lys Glu Lys Ile Gln Glu Met Phe Glu Glu Tyr
340 345

<210> 248

<211> 328

<212> PRT

<213> Helicobacter pylori

<400> 248

Met Asp Phe Lys Asn Lys Lys Trp Leu Phe Leu Ala Pro Leu Ala Gly
1 5 10 15

Tyr Thr Asp Leu Pro Phe Arg Ser Val Val Lys Lys Phe Gly Val Asp
20 25 30

Val Thr Thr Ser Glu Met Val Ser Ser His Ser Leu Val Tyr Ala Phe
35 40 45

Asp Lys Thr Ser Lys Met Leu Glu Lys Ser Pro Leu Glu Asp His Phe
50 55 60

Met Ala Gln Ile Ser Gly Ser Lys Glu Ser Val Val Lys Glu Ala Val
65 70 75 80

Glu Lys Ile Asn Ala Leu Glu His Val Asn Gly Ile Asp Phe Asn Cys
85 90 95

Gly Cys Pro Ala Pro Lys Val Ala Asn His Gly Asn Gly Ser Gly Leu
100 105 110

```
Leu Lys Asp Leu Asn His Leu Val Lys Leu Leu Lys Thr Ile Arg Glu
        115                 120                 125

Asn Thr Ser Lys Lys Ile Thr Ser Val Lys Val Arg Leu Gly Phe Glu
    130                 135                 140

Lys Lys Ile Pro Lys Glu Ile Ala His Ala Leu Asn Asp Ala Pro Val
145                 150                 155                 160

Asp Tyr Val Val Val His Gly Arg Thr Arg Ser Asp Lys Tyr Gln Lys
                165                 170                 175

Asp Lys Ile Asp Tyr Glu Ser Ile Ala Leu Met Lys Lys Ile Leu Lys
            180                 185                 190

Lys Pro Val Ile Ala Asn Gly Glu Ile Asp Ser Val Lys Lys Ala Phe
        195                 200                 205

Glu Val Leu Gln Ile Thr Gln Ala Asp Gly Leu Met Ile Gly Arg Ala
    210                 215                 220

Ala Leu Arg Ala Pro Trp Ile Phe Trp Gln Ile Arg Asn Asn Thr Thr
225                 230                 235                 240

Lys Leu Pro Ala Val Val Lys Lys Asp Leu Val Leu Glu His Phe Asp
                245                 250                 255

Lys Met Val Glu Phe Tyr Gly Asp Met Gly Val Ile Met Phe Arg Lys
            260                 265                 270

Asn Leu His Ala Tyr Ala Lys Gly Glu Met Gln Ala Ser Ala Phe Arg
        275                 280                 285

Asn Cys Val Asn Thr Leu Thr Glu Ile Lys Ser Met Arg Glu Ser Ile
    290                 295                 300

Glu Glu Phe Phe Asn Gln Glu Met Leu Gln Ser Glu Val Pro Leu Trp
305                 310                 315                 320

Val Glu Leu Asn Gln Lys Ser Val
                325
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<210> 249

<211> 674

<212> PRT

<213> Helicobacter pylori

<400> 249

Met Ala Ile Gly Ser Leu Ser Ser Leu Gly Leu Gly Ser Lys Val Leu
1   5   10   15

Asn Tyr Asp Val Ile Asp Lys Leu Lys Asp Ala Asp Glu Lys Ala Leu
            20   25   30

Ile Ala Pro Leu Asp Lys Lys Met Glu Gln Asn Val Glu Lys Gln Lys
        35   40   45

Ala Leu Val Glu Ile Lys Thr Leu Leu Ser Ala Leu Lys Gly Pro Val
    50   55   60

Lys Thr Leu Ser Asp Tyr Ser Thr Tyr Ile Ser Arg Lys Ser Asn Val
65   70   75   80

Thr Gly Asp Ala Leu Ser Ala Ser Val Gly Val Gly Val Pro Ile Gln
                85   90   95

Asp Ile Lys Val Asp Val Gln Asn Leu Ala Gln Gly Asp Ile Asn Glu
            100   105   110

Leu Gly Ala Lys Phe Ser Ser Arg Asp Asp Ile Phe Ser Gln Val Asp
        115   120   125

Thr Thr Leu Lys Phe Tyr Thr Gln Asn Lys Asp Tyr Ala Val Asn Ile
    130   135   140

Lys Ala Gly Met Thr Leu Gly Asp Val Ala Gln Ser Ile Thr Asp Ala
145   150   155   160

Thr Asn Gly Glu Val Met Gly Ile Val Met Lys Thr Gly Gly Asn Asp
                165   170   175

Pro Tyr Gln Leu Met Val Asn Thr Lys Asn Thr Gly Glu Asp Asn Arg
            180   185   190

Val Tyr Phe Gly Ser His Leu Gln Ser Thr Leu Thr Asn Lys Asn Ala
        195   200   205

Leu Ser Leu Gly Val Asp Gly Ser Gly Lys Ser Glu Val Ser Leu Asn
    210   215   220

Leu Lys Gly Ala Asp Gly Asn Met His Glu Val Pro Ile Met Leu Glu
225   230   235   240

Leu Pro Glu Ser Ala Ser Ile Lys Gln Lys Asn Thr Ala Ile Gln Lys
                245   250   255

Ala Met Glu Gln Ala Leu Glu Asn Asp Pro Asn Phe Lys Asn Leu Ile
            260   265   270

Ala Asn Gly Asp Ile Ser Ile Asp Thr Leu His Gly Gly Glu Ser Leu
275 280 285

Ile Ile Asn Asp Arg Arg Gly Gly Asn Ile Glu Val Lys Gly Ser Lys
290 295 300

Ala Lys Glu Leu Gly Phe Leu Gln Thr Thr Thr Gln Glu Ser Asp Leu
305 310 315 320

Leu Lys Ser Ser Arg Thr Ile Lys Glu Gly Lys Leu Glu Gly Val Val
325 330 335

Ser Leu Asn Gly Gln Lys Leu Asp Leu Ser Ala Leu Thr Lys Glu Ser
340 345 350

Asn Thr Ser Glu Glu Asn Thr Asp Ala Ile Ile Gln Ala Ile Asn Ala
355 360 365

Lys Glu Gly Leu Ser Ala Phe Lys Asn Ala Glu Gly Lys Leu Val Ile
370 375 380

Asn Ser Lys Thr Gly Met Leu Thr Ile Lys Gly Glu Asp Ala Leu Gly
385 390 395 400

Lys Ala Ser Leu Lys Asp Leu Gly Leu Asn Ala Gly Met Val Gln Ser
405 410 415

Tyr Glu Ala Ser Gln Asn Thr Leu Phe Met Ser Lys Asn Leu Gln Lys
420 425 430

Ala Ser Asp Ser Ala Phe Thr Tyr Asn Gly Val Ser Ile Thr Arg Pro
435 440 445

Thr Asn Glu Val Asn Asp Val Ile Ser Gly Val Asn Ile Thr Leu Glu
450 455 460

Gln Thr Thr Glu Pro Asn Lys Pro Ala Ile Ile Ser Val Ser Arg Asp
465 470 475 480

Asn Gln Ala Ile Ile Asp Ser Leu Thr Glu Phe Val Lys Ala Tyr Asn
485 490 495

Glu Leu Ile Pro Lys Leu Asp Glu Asp Thr Arg Tyr Asp Ala Asp Thr
500 505 510

Lys Ile Ala Gly Ile Phe Asn Gly Val Gly Asp Ile Arg Ala Ile Arg
515 520 525

Ser Ser Leu Asn Asn Val Phe Ser Tyr Ser Val His Thr Asp Asn Gly
530 535 540

Val Glu Ser Leu Met Lys Tyr Gly Leu Ser Leu Asp Asp Lys Gly Val
545 550 555 560

Met Ser Leu Asp Glu Ala Lys Leu Ser Ser Ala Leu Asn Ser Asn Pro
565 570 575

Lys Ala Thr Gln Asp Phe Phe Tyr Gly Ser Asp Ser Lys Asp Met Gly
580 585 590

Gly Arg Glu Ile His Gln Glu Gly Ile Phe Ser Lys Phe Asn Gln Val
595 600 605

Ile Ala Asn Leu Ile Asp Gly Gly Asn Ala Lys Leu Lys Ile Tyr Glu
610 615 620

Asp Ser Leu Asp Arg Asp Ala Lys Ser Leu Thr Lys Asp Lys Glu Asn
625 630 635 640

Ala Gln Glu Leu Leu Lys Thr Arg Tyr Asn Ile Met Ala Asp Val Leu
645 650 655

Pro Leu Met Ile Ala Lys Ser Leu Lys Pro Ile Lys Asn Ser Ile Pro
660 665 670

Cys Lys

<210> 250

<211> 462

<212> PRT

<213> Helicobacter pylori

<400> 250

Met Gln Ile Ala Thr Ala Ile Trp Lys Thr Arg Ile Trp Gln Leu Gln
1 5 10 15

Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu Glu Ala Gln
20 25 30

His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu Lys Glu Lys
35 40 45

Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Gln Glu Lys Glu Asn
50 55 60

Phe Lys Lys Gln Arg Ala Val Cys Lys Glu Ser Gln Ala Lys Ala Leu
65 70 75 80

Asp Ala Met Leu Asn Tyr Met Ala Tyr Thr Lys Asp Glu Ile Lys Ser
85 90 95

Met Ile Leu Glu Gln Leu Glu Glu Glu Leu Glu Ala Gln Lys Ser Ala
100 105 110

Leu Ile Arg Arg Tyr Glu Lys Glu Ala Lys Glu Glu Gly Lys Lys Lys
115 120 125

Ser Tyr Ala Ile Leu Ala Glu Ala Thr Ala Arg Phe Ala Gly Asn Tyr
130 135 140

Ala Ala Glu Asn Leu Thr Thr Arg Ile Ala Leu Pro Cys Ser Asp Tyr
145 150 155 160

Ile Gly Arg Val Ile Gly Lys Asp Gly Lys Asn Ile Glu Ala Phe Lys
165 170 175

Lys Val Ser Gly Val Asp Ile Glu Phe Ser Glu Asp Ser Ser Glu Leu
180 185 190

Cys Leu Ser Ser Phe Asn Leu Tyr Arg Arg Glu Val Ala Ser Glu Thr
195 200 205

Leu Lys Ile Leu Ile Glu Asp Gly Arg Ile Gln Pro Asn Arg Ile Glu
210 215 220

Glu Val Tyr His Arg Val Ala Arg Asn Leu Glu Lys Glu Leu Leu Ser
225 230 235 240

Glu Gly Glu Ser Val Val Leu Glu Leu Glu Leu Gly Ala Met Glu Asp
245 250 255

Glu Leu Lys Ile Leu Ile Gly Lys Met Arg Tyr Arg Ser Ser Phe Gly
260 265 270

Gln Asn Ala Leu Gln His Ser Lys Glu Val Ala Leu Leu Ala Gly Leu
275 280 285

Ile Ala Glu Gln Leu Gly Gly Asp Lys Lys Leu Ala Arg Arg Ala Gly
290 295 300

Ile Leu His Asp Ile Gly Lys Ala Leu Thr Gln Glu Leu Gly Arg Asp
305 310 315 320

His Val Asn Leu Gly Val Glu Val Cys Lys Arg His Lys Glu Asp Pro
325 330 335

Val Val Ile Asn Ala Ile Tyr Ala His His Gly His Glu Glu Ile Leu
340 345 350

Ser Val Glu Cys Ala Ser Val Cys Ala Ala Asp Ala Leu Ser Ala Gly
        355   360   365

Arg Pro Gly Ala Arg Arg Lys Ser Asp Glu Glu Tyr Ala Lys Arg Met
    370   375   380

Gln Ala Leu Glu Glu Ile Ala Leu Glu Phe Asp Gly Val Glu Lys Ala
385   390   395   400

Tyr Ala Met Glu Ser Gly Arg Glu Leu Arg Val Ile Val Lys Ser Asn
                405   410   415

Gln Val Arg Asp Asn Gln Val Pro Ile Ile Ala Arg Lys Ile Ala Lys
            420   425   430

Lys Ile Glu Glu Ser Ala Gln Tyr Val Gly Glu Val Gly Val Gln Val
        435   440   445

Val Arg Glu Ser Arg Phe Lys Thr Thr Ala Thr Leu Lys Gln
    450   455   460

<210> 251

<211> 119

<212> PRT

<213> Helicobacter pylori

<400> 251

Met Pro Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu
1   5   10   15

Val Ala Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn
            20   25   30

Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro
        35   40   45

Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu
    50   55   60

Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn
65   70   75   80

Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val
                85   90   95

Ile Glu Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe
            100   105   110

His Pro Leu Lys Pro Trp Leu
115

<210> 252

<211> 527

<212> PRT

<213> Helicobacter pylori

<400> 252

Met Glu Asn Asn Pro Asn Asn Asn Gln Ala Ser Leu Glu Arg Asn Glu
1 5 10 15

Leu His Asn Thr Ile Trp Lys Val Ala Asn Glu Leu Arg Gly Ser Val
20 25 30

Asp Gly Trp Asp Phe Lys Gln Tyr Val Leu Gly Ile Leu Phe Tyr Arg
35 40 45

Tyr Ile Ser Glu Asn Met Thr His Tyr Ile Asn Lys Glu Glu Arg Lys
50 55 60

Arg Asp Pro Ser Phe Asp Tyr Ala Lys Leu Ser Asp Glu Lys Ala Glu
65 70 75 80

Arg Gly Arg Lys His Leu Ile Glu Gln Lys Gly Phe Phe Ile Pro Pro
85 90 95

Ser Ala Leu Phe Cys Asn Ala Leu Lys Asn Ala Cys His Asn Glu Asp
100 105 110

Leu Asn Val Thr Leu Gln Asn Ile Phe Asn Glu Ile Glu Lys Ser Ser
115 120 125

Leu Gly Thr Pro Ser Glu Glu Asn Val Lys Gly Leu Phe Ala Asp Leu
130 135 140

Asp Val Asn Ser Asn Lys Leu Gly Ser Ser His Gln Asn Arg Val Glu
145 150 155 160

Lys Leu Thr Lys Ile Leu Glu Ala Ile Gly Gly Met Gln Leu Gly Asp
165 170 175

Tyr Leu Lys Ser Gly Ile Asp Val Phe Gly Asp Ala Tyr Glu Tyr Leu
180 185 190

Met Ala Met Tyr Ala Ser Asn Ala Gly Lys Ser Gly Gly Glu Phe Phe
195 200 205

Thr Pro Gln Glu Val Ser Glu Leu Leu Ala Lys Ile Thr Leu His Gly
    210   215   220

Gln Glu Ser Val Asn Lys Val Tyr Asp Pro Cys Cys Gly Ser Gly Ser
225   230   235   240

Leu Leu Leu Gln Phe Ser Lys Val Leu Gly Asp Lys Asn Val Ser Lys
                245   250   255

Gly Tyr Phe Gly Gln Glu Ile Asn Leu Thr Thr Tyr Asn Leu Cys Arg
            260   265   270

Ile Asn Met Phe Leu His Asp Ile Asn Tyr Ser Lys Phe His Ile Ala
        275   280   285

His Gly Asp Thr Leu Leu Asp Pro Lys His Glu Asp Asp Glu Pro Phe
    290   295   300

Asp Ala Ile Val Ser Asn Pro Pro Tyr Ser Thr Lys Trp Val Gly Asp
305   310   315   320

Ser Asn Pro Ile Leu Ile Asn Asp Glu Arg Phe Ser Pro Ala Gly Val
                325   330   335

Leu Ala Pro Lys Asn Ala Ala Asp Leu Ala Phe Thr Met His Met Leu
            340   345   350

Ser Tyr Leu Ser Asn Ser Gly Thr Ala Ala Ile Val Glu Phe Pro Gly
        355   360   365

Val Leu Tyr Arg Gly Asn Ala Glu Ala Lys Ile Arg Glu Tyr Leu Val
    370   375   380

Lys Glu Asn Val Ile Asp Cys Val Ile Ala Leu Pro Asp Asn Leu Phe
385   390   395   400

Phe Gly Thr Ser Ile Ala Thr Cys Ile Leu Val Leu Lys Lys Asn Lys
                405   410   415

Gln Asp Asp Thr Thr Leu Phe Ile Asp Ala Ser Lys Glu Phe Val Lys
            420   425   430

Glu Gly Lys Lys Asn Lys Leu Lys Glu Arg Asn Arg Glu Lys Ile Leu
        435   440   445

Gln Thr Tyr Ile Glu Arg Lys Glu Ile Lys His Phe Cys Ala Leu Ala
    450   455   460

Asn Ile Glu Lys Ile Lys Glu Asn Asp Tyr Asn Leu Ser Val Asn Arg
465   470   475   480

Tyr Val Glu Gln Glu Asp Thr Lys Glu Ala Ile Asp Ile Lys Ala Leu
485 490 495

Asn Ser Glu Ile Ala Gln Ile Val Glu Lys Gln Ser Ala Leu Arg Asn
500 505 510

Arg Leu Glu Ser Ile Ile Lys Glu Leu Glu Gly Gly Gln Asn Ala
515 520 525

<210> 253

<211> 533

<212> PRT

<213> Helicobacter pylori

<400> 253

Met Leu Gln Thr Ile Asn Leu Thr Gln Arg Tyr Ala Thr Lys Lys Leu
1 5 10 15

Phe Glu Asn Val Asn Ile Lys Leu Asp Lys Asn Lys Arg Tyr Gly Leu
20 25 30

Ile Gly Ala Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ser
35 40 45

Lys Ser Ile Asp Cys Ser Ser Gly Glu Val Ile Ile Thr Ser Gly Met
50 55 60

Lys Met Gly Val Leu Gly Gln Asp Gln Tyr Ala Phe Glu Asp Leu Ser
65 70 75 80

Leu Lys Asp Ala Val Leu Ile Gly Asn Lys Arg Leu Tyr Asp Ala Ile
85 90 95

Lys Glu Lys Glu Arg Leu Tyr Thr Glu Gly Asp Leu Ser Asp Asp Lys
100 105 110

Val Asn Ala Arg Leu Gly Glu Leu Glu Thr Ile Cys Val Glu Glu Asp
115 120 125

Pro Met Tyr Glu Cys Glu Val Ala Ile Glu Lys Ile Leu Glu Asp Leu
130 135 140

Gly Ile Pro Ser Ser Lys His Asn Asp Leu Met Lys Thr Leu Pro Ser
145 150 155 160

Ser Asp Lys Phe Lys Ile Leu Leu Ala Gln Val Leu Phe Pro Lys Pro
165 170 175

Asp Ile Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala
180 185 190

Ile Glu Trp Leu Glu Asn Asn Leu Lys Arg His Glu Gly Thr Met Val
195 200 205

Val Ile Ser His Asp Arg His Phe Leu Asn Ala Val Cys Thr His Ile
210 215 220

Leu Asp Leu Asp Phe His Ser Val Arg Glu Phe Ser Gly Asn Tyr Asp
225 230 235 240

Asp Trp Tyr Ile Ala Ser Thr Leu Ile Ala Lys Gln Gln Glu Ala Glu
245 250 255

Arg Asn Lys Lys Leu Lys Glu Lys Glu Glu Leu Glu Lys Phe Ile Ala
260 265 270

Arg Phe Ser Ala Asn Ala Ser Lys Ala Lys Gln Ala Thr Ser Arg Gln
275 280 285

Lys Gln Leu Asp Lys Leu Asp Ile Gln Ser Leu Ala Val Ser Ser Arg
290 295 300

Arg Asp Pro Ser Ile Ile Phe Lys Pro Lys Arg Thr Ile Gly Asn Glu
305 310 315 320

Ala Leu Glu Cys Glu Asn Ile Ser Lys Ser Tyr Asp Asp Gln Ile Val
325 330 335

Leu Asn Gln Val Ser Leu Lys Val Met Pro Lys Asp Lys Ile Ala Leu
340 345 350

Ile Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Cys Lys Ile Leu Val
355 360 365

Glu Glu Leu Lys Pro Asp Lys Gly Val Val Lys Trp Gly Ala Thr Val
370 375 380

Ser Lys Gly Tyr Phe Pro Gln Asn Val Ser Glu Glu Ile Ser Gly Glu
385 390 395 400

Glu Thr Leu Tyr Gln Trp Leu Phe Asn Phe Asn Lys Lys Ile Glu Ser
405 410 415

Ala Glu Val Arg Asn Ala Leu Gly Arg Met Leu Phe Asn Gly Glu Glu
420 425 430

Gln Glu Lys Cys Val Asn Ala Leu Ser Gly Gly Glu Lys His Arg Met
435 440 445

Val Leu Ser Lys Leu Met Leu Glu Gly Gly Asn Phe Leu Val Leu Asp
450 455 460

Glu Pro Thr Asn His Leu Asp Leu Glu Ala Ile Ile Ala Leu Gly Glu
465 470 475 480

Ala Leu Phe Lys Phe Asp Gly Ala Leu Ile Cys Val Ser His Asp Arg
485 490 495

Glu Leu Ile Asp Ala Tyr Ala Asn Arg Ile Ile Glu Leu Val Pro Ser
500 505 510

Pro Lys Gly Ala Ser Ile Ile Asp Phe Lys Gly Ser Tyr Glu Glu Tyr
515 520 525

Leu Ala Ser Lys Lys
530

<210> 254

<211> 542

<212> PRT

<213> Helicobacter pylori

<400> 254

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Val Phe Ser
1 5 10 15

Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
20 25 30

Gly Glu Ala Tyr Phe Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser
35 40 45

Asn Arg Tyr Gly Ala Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys
50 55 60

Gly Leu Thr Gln Leu Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser
65 70 75 80

Phe Leu Asn Glu Ser Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu
85 90 95

Asn Lys Ile Asp Lys Lys Thr Asn Lys Ser Lys Val Ala Lys Thr Glu
100 105 110

Glu Thr Glu Leu Lys Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys
115 120 125

Val Cys His Gln Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln
130 135 140

Gln Ser Ile Val Ile Pro Leu Glu Thr Phe Ala Leu Ser Ala Ser Val
145 150 155 160

Lys Gly Asn Leu Leu Ala Val Val Leu Ala Asp Asn Ser Ala Asn Leu
165 170 175

Tyr Asp Ile Thr Ser Gln Lys Leu Leu Phe Ser Glu Lys Gly Ser Pro
180 185 190

Ser Thr Thr Ile Asn Ser Leu Met Ala Met Pro Ile Phe Met Asp Thr
195 200 205

Val Val Val Phe Pro Met Leu Asp Gly Arg Leu Leu Val Val Asp Tyr
210 215 220

Val His Gly Asn Pro Thr Pro Ile Arg Asn Ile Val Ile Ser Ser Asp
225 230 235 240

Lys Phe Phe Asn Asn Ile Thr Tyr Leu Ile Val Asp Gly Asn Asn Met
245 250 255

Ile Ala Ser Thr Gly Lys Arg Ile Leu Ser Val Val Ser Gly Gln Glu
260 265 270

Phe Asn Tyr Asp Gly Asp Ile Val Asp Leu Leu Tyr Asp Lys Gly Thr
275 280 285

Leu Tyr Val Leu Thr Leu Asp Gly Gln Ile Leu Gln Met Asp Lys Ser
290 295 300

Leu Arg Glu Leu Asn Ser Val Lys Leu Pro Ser Ser Leu Asn Thr Ile
305 310 315 320

Val Leu Asn His Asn Lys Leu Tyr Ser Leu Glu Lys Arg Gly Tyr Val
325 330 335

Ile Glu Val Asp Leu Asn Asp Phe Asp Ser Tyr Asn Val Tyr Lys Thr
340 345 350

Pro Thr Ile Gly Ser Phe Lys Phe Phe Ser Ser Asn Arg Leu Asp Lys
355 360 365

Gly Val Phe Tyr Asp Lys Asn Arg Val Tyr Tyr Asp Arg Tyr Tyr Leu
370 375 380

Asp Tyr Asn Asp Phe Lys Pro Lys Leu Tyr Pro Val Val Glu Lys Ser
385 390 395 400

Ala Ser Lys Lys Ser Gln Lys Gly Glu Lys Gly Asn Ala Pro Ile Tyr
405 410 415

Leu Gln Glu Arg His Lys Ala Lys Glu Asn Lys Gln Pro Leu Glu Glu
420 425 430

Asn Lys Val Lys Pro Arg Asn Ser Gly Phe Glu Glu Glu Glu Val Lys
435 440 445

Thr Arg Arg Pro Glu Pro Ile Arg Asp Gln Asn Asn Ala Thr Gln Gln
450 455 460

Gly Glu Thr Lys Asn Asn Glu Ser Lys Asn Ala Pro Val Leu Lys Glu
465 470 475 480

Asn Ala Ala Lys Lys Glu Val Pro Lys Pro Asn Ser Lys Glu Glu Lys
485 490 495

Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala Glu Gln Arg Ala
500 505 510

Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu Arg Asp Glu Lys
515 520 525

Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Met Asn Lys Lys
530 535 540

<210> 255

<211> 291

<212> PRT

<213> Helicobacter pylori

<400> 255

Met Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly
1 5 10 15

Ala Val Leu Gly Ala Gln Ile Leu Gln Ala Glu Glu Ser Lys Gly Ser
20 25 30

Val Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser
35 40 45

Ala Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser
50 55 60

Asn Val His Leu Gln Gly Asn His Ala Ser Tyr Lys Ser Met Leu Asn
65 70 75 80

Phe Gly Val Pro Tyr Leu Gln Val Asp Phe Leu Lys Ser Thr Gln Lys
                85   90   95

Lys Gln Val His Leu Ser Tyr Glu Ile Ala Ser Tyr Gln Leu Asn Glu
            100   105   110

Arg Leu Phe Glu Thr Ser Asp Phe Val Ala Met Gly Arg Tyr Glu Arg
        115   120   125

Asp Asp Ala Ser Val Ala Asn Ile Ala Asn Gln Leu Lys Gly Thr Thr
    130   135   140

Pro Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met
145   150   155   160

Pro Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg
                165   170   175

Glu Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val
            180   185   190

Ser Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu
        195   200   205

Lys Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val
    210   215   220

Tyr Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys
225   230   235   240

Glu Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser
                245   250   255

Ala Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg
            260   265   270

Asp Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr
        275   280   285

Thr Ile Val
    290

<210> 256

<211> 505

<212> PRT

<213> Helicobacter pylori

<400> 256

Met Val Asn Lys Asp Val Lys Gln Thr Thr Ala Phe Gly Ala Pro Val
1   5   10   15

Trp Asp Asp Asn Asn Val Ile Thr Ala Gly Pro Arg Gly Pro Val Leu
            20   25   30

Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala Phe Asp Arg Glu
        35   40   45

Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser Gly Ala Tyr Gly
    50   55   60

Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr Lys Ala Lys Ile
65   70   75   80

Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe Arg Phe Ser Thr
                85   90   95

Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg Asp Pro Arg Gly
            100   105   110

Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp Asp Leu Val Gly
        115   120   125

Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile Lys Phe Pro Asp
    130   135   140

Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn Leu Pro Asn His
145   150   155   160

Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu Ser Leu Tyr Gln
                165   170   175

Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys Ser Phe Arg His
            180   185   190

Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile Asn Ala Lys Gly
        195   200   205

Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met Gln Gly Val Lys
    210   215   220

His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys Tyr Asp Pro Asp
225   230   235   240

Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg Gly Asp Phe Pro
                245   250   255

Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu Asp Ala Lys Lys
            260   265   270

Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp Tyr Leu Gln Asp
275 280 285

Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn Lys Asn Pro Glu
290 295 300

Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser Pro Ala Asn Val
305 310 315 320

Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu Gln Gly Arg Leu
325 330 335

Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly Val Asn Tyr Pro
340 345 350

Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His Ser Ser Ser Arg
355 360 365

Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu Gln Asn Tyr Thr
370 375 380

Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser Ala Arg Asp Pro
385 390 395 400

Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu Val Trp Asn Trp
405 410 415

Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln Pro Gly Asp Tyr
420 425 430

Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu His Asp Thr Ile
435 440 445

Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile Val Asp Lys Gln
450 455 460

Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala Glu Gly Val Lys
465 470 475 480

Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp Met His Gly Lys
485 490 495

Asp Met His His Thr Lys Lys Lys Lys
500 505

<210> 257

<211> 791

<212> PRT

<213> Helicobacter pylori

<400> 257

Met Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro
1   5   10   15

Leu Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val
            20   25   30

Thr Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val
        35   40   45

Thr Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu
    50   55   60

Phe Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly
65   70   75   80

Gln Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr
                85   90   95

Val Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn
            100   105   110

Thr Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly
        115   120   125

Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys
    130   135   140

Met Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr
145   150   155   160

Ala Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu
                165   170   175

Thr Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr
            180   185   190

Tyr Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met
        195   200   205

Lys Asn Leu Phe Asn Pro Thr Gln Ala Asp Lys Glu Pro Gly Thr Pro
    210   215   220

Ser Glu Gln Asn Asn Ala Leu Ile Lys Met Asn Gly Tyr Leu Ser Asp
225   230   235   240

Arg Asp Thr Leu Thr Phe Ser Trp Asn Met Thr Arg Asp Asn Ala Thr
                245   250   255

Arg Pro Leu Arg Ser Asn Ala Ile Gly Leu Ala Tyr Pro Cys Glu Ala
260 265 270

Pro Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser
275 280 285

Phe Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser
290 295 300

Leu Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu
305 310 315 320

Asp Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu
325 330 335

Phe Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser
340 345 350

Ala Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr
355 360 365

Pro Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu
370 375 380

Phe Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp
385 390 395 400

Glu Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu
405 410 415

Ser Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn
420 425 430

Gln Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu
435 440 445

Val Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala
450 455 460

Asn Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His
465 470 475 480

Lys Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu
485 490 495

Tyr Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser
500 505 510

Ala Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr
515 520 525

Tyr Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met
530 535 540

Arg Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly
545 550 555 560

Ser Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly
565 570 575

Arg Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr
580 585 590

Ala Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr
595 600 605

Gly Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn
610 615 620

Val Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala
625 630 635 640

Asp Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys
645 650 655

Leu Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser
660 665 670

Arg Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro
675 680 685

Asp Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys
690 695 700

Cys Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly
705 710 715 720

Val Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp
725 730 735

Lys Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe
740 745 750

Tyr Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly
755 760 765

Thr Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg
770 775 780

Phe Glu Val Ala Tyr Lys Trp
785 790

<210> 258

<211> 1290

<212> PRT

<213> Helicobacter pylori

<400> 258

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
1   5   10   15

Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His
            20   25   30

Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
        35   40   45

Ala Thr Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly
    50   55   60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65   70   75   80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
                85   90   95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
            100   105   110

Trp Asp Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln
        115   120   125

Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn
    130   135   140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145   150   155   160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
                165   170   175

Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
            180   185   190

Lys Asn Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly
        195   200   205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
    210   215   220

Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
225 230 235 240

Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn
245 250 255

Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
260 265 270

Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
275 280 285

His Leu Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala
290 295 300

Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
305 310 315 320

Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys
325 330 335

Asp Lys Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln
340 345 350

Asn Ser Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn
355 360 365

Ser Ala Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro
370 375 380

Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr
385 390 395 400

Asn Ala Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr
405 410 415

Thr Asn Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser
420 425 430

Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn
435 440 445

Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr
450 455 460

Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp
465 470 475 480

Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg
485 490 495

Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile
500 505 510

Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr
515 520 525

Gly Lys Val Asn Ile Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala
530 535 540

Val Lys Asn Phe Asn Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val
545 550 555 560

Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser
565 570 575

Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser
580 585 590

Gly Gly Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe
595 600 605

Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val
610 615 620

Glu Ile Thr Arg Lys Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly
625 630 635 640

Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val
645 650 655

Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile
660 665 670

Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala
675 680 685

Thr Leu Asn Val Gly Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val
690 695 700

Asp Ser Ala Thr Gly Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala
705 710 715 720

Gln Asp Leu Ile Lys Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile
725 730 735

Ile Gly Tyr Gly Asn Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val
740 745 750

Asn Leu Ile Glu Gln Phe Lys Glu Arg Leu Ala Leu Tyr Asn Asn Asn
755 760 765

Asn Arg Met Asp Ile Cys Val Val Arg Asn Thr Asp Asp Ile Lys Ala
770 775 780

Cys Gly Thr Ala Ile Gly Asn Gln Ser Met Val Asn Asn Pro Asp Asn
785 790 795 800

Tyr Lys Tyr Leu Ile Gly Lys Ala Trp Lys Asn Ile Gly Ile Ser Lys
805 810 815

Thr Ala Asn Gly Ser Lys Ile Ser Val Tyr Tyr Leu Gly Asn Ser Thr
820 825 830

Pro Thr Glu Lys Gly Gly Asn Thr Thr Asn Leu Pro Thr Asn Thr Thr
835 840 845

Ser Asn Val Arg Ser Ala Asn Asn Ala Leu Ala Gln Asn Ala Pro Phe
850 855 860

Ala Gln Pro Ser Ala Thr Pro Asn Leu Val Ala Ile Asn Gln His Asp
865 870 875 880

Phe Gly Thr Ile Glu Ser Val Phe Glu Leu Ala Asn Arg Ser Lys Asp
885 890 895

Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln Gly Arg Asp Leu Leu
900 905 910

Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly Tyr Ala Arg Gln Met
915 920 925

Ile Asp Asn Thr Ser Thr Gly Glu Ile Thr Lys Gln Leu Asn Ala Ala
930 935 940

Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu His Lys Thr Ser Ser
945 950 955 960

Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile Leu Asn Ser Arg Leu
965 970 975

Val Asn Leu Ser Arg Arg His Thr Asn Asn Ile Asp Ser Phe Ala Gln
980 985 990

Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala Ser Leu Glu Ser Ala
995 1000 1005

Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr Glu Lys Pro Thr
1010 1015 1020

Asn Val Trp Ala Asn Ala Ile Gly Gly Thr Ser Leu Asn Asn Gly
1025 1030 1035

Gly Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp Ala Tyr
1040 1045 1050

Leu Asn Gly Glu Val Glu Ala Ile Val Gly Gly Phe Gly Ser Tyr
1055 1060 1065

Gly Tyr Ser Ser Phe Asn Asn Gln Ala Asn Ser Leu Asn Ser Gly
1070 1075 1080

Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn
1085 1090 1095

Gln His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp
1100 1105 1110

Gln Ser Ser Leu Asn Phe Lys Ser Ala Leu Leu Arg Asp Leu Asn
1115 1120 1125

Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala Ala Thr Arg Ala Ser
1130 1135 1140

Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys
1145 1150 1155

Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser Thr Asn Phe
1160 1165 1170

Lys Ser Asn Ser Asn Gln Val Ala Leu Lys Asn Gly Ser Ser Ser
1175 1180 1185

Gln His Leu Phe Asn Ala Ser Ala Asn Val Glu Ala Arg Tyr Tyr
1190 1195 1200

Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val Leu Gln
1205 1210 1215

Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn Thr
1220 1225 1230

Phe Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg
1235 1240 1245

Val Met Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu
1250 1255 1260

Asn Leu Gly Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly
1265 1270 1275

His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
1280 1285 1290

<210> 259

<211> 174

<212> PRT

<213> Helicobacter pylori

<400> 259

Met Pro Gln Ile Gln Ser Ser His Ser Asn His Phe Asp Phe Thr Ile
1 5 10 15

Asp Thr Ala Asp Arg Thr Lys Leu Leu Met Ser Tyr Leu Val Val Pro
20 25 30

Thr Thr Ala Asn Phe Asn Asn Val Met His Gly Gly Glu Leu Leu Asn
35 40 45

Leu Leu Asp Lys Val Ala Tyr Val Cys Ser Thr Arg Tyr Cys Ala Lys
50 55 60

Gly Thr Val Thr Leu Ser Val Asp Gly Val Thr Phe Lys Tyr Pro Ile
65 70 75 80

Pro Val Gly Asn Leu Leu Thr Phe Leu Ala Ser Ile Asn Tyr Val Gly
85 90 95

Asn Thr Ser Cys Glu Val Gly Ile Lys Val Leu Ser Glu Asp Ile Lys
100 105 110

Thr Arg Glu Ile Thr His Thr Asn Ser Cys Tyr Phe Thr Met Val Ala
115 120 125

Val Glu Asn Gly Lys Pro Thr Pro Met Pro Lys Tyr Glu Pro Lys Thr
130 135 140

Glu Val Glu Ile Arg Arg Tyr Glu Gly Ala Leu Lys Arg Lys Glu Met
145 150 155 160

Arg Thr Arg Gly Tyr Leu Lys Ser Gly Lys His Glu Gly Val
165 170

<210> 260

<211> 379

<212> PRT

<213> Helicobacter pylori

<400> 260

Leu Asn Asn Leu Asp Ile Lys Thr Leu Gly Gln Val Phe Thr Pro Lys
1   5   10   15

Lys Ile Val Asp Phe Met Leu Thr Leu Lys His Asn His Gly Ser Val
            20   25   30

Leu Glu Pro Ser Ala Gly Asp Gly Ser Phe Leu Lys Arg Leu Lys Lys
        35   40   45

Ala Val Arg Ile Glu Ile Asp Pro Lys Ile Cys Pro Lys Asn Ala Leu
    50   55   60

Cys Met Asp Phe Phe Asp Tyr Pro Leu Glu Asn Gln Phe Asp Thr Ile
65   70   75   80

Ile Gly Asn Pro Pro Tyr Val Lys His Lys Asp Ile Ala Pro Ser Thr
                85   90   95

Lys Glu Lys Leu His Tyr Ser Leu Phe Asp Glu Arg Ser Asn Leu Tyr
            100   105   110

Leu Phe Phe Ile Glu Lys Ala Ile Lys His Leu Lys Pro Lys Gly Glu
        115   120   125

Leu Ile Phe Ile Thr Pro Arg Asp Phe Leu Lys Ser Thr Ser Ser Val
    130   135   140

Lys Leu Asn Glu Trp Ile Tyr Lys Glu Gly Thr Ile Thr His Phe Phe
145   150   155   160

Glu Leu Gly Asp Gln Lys Val Phe Pro Asn Ala Met Pro Asn Cys Val
                165   170   175

Ile Phe Arg Phe Cys Lys Gly Asn Phe Ser Arg Ile Thr Asn Asp Gly
            180   185   190

Leu Gln Phe Leu Cys Lys Lys Gly Ile Leu Tyr Phe Leu Asn Gln Ser
        195   200   205

Tyr Thr Gln Lys Leu Ser Glu Val Phe Lys Val Lys Val Gly Ala Val
    210   215   220

Ser Gly Cys Asp Lys Ile Phe Lys Asn Glu Lys Tyr Gly Asn Leu Glu
225   230   235   240

Phe Val Thr Ser Ile Thr Lys Arg Thr Asn Ala Leu Glu Lys Met Val
                245   250   255

Phe Val Asn Glu Pro Asn Asp Tyr Leu Leu Gln His Lys Asp Ser Leu
            260   265   270

Met Gln Arg Lys Ile Lys Lys Phe Asn Glu Asn Asn Trp Phe Glu Trp
275 280 285

Gly Arg Met His His Ile Ser Pro Lys Lys Arg Ile Tyr Val Asn Ala
290 295 300

Lys Thr His Gln Lys Asn Pro Phe Phe Ile His Gln Cys Pro Asn Tyr
305 310 315 320

Asp Gly Ser Ile Leu Ala Leu Phe Pro Tyr Asn Gln Asn Leu Asp Leu
325 330 335

Gln Asn Leu Cys Asp Lys Leu Asn Ala Ile Asn Trp Gln Glu Leu Gly
340 345 350

Phe Val Cys Gly Gly Arg Phe Leu Phe Ser Gln Arg Ser Leu Glu Asn
355 360 365

Ala Leu Leu Pro Lys Asp Phe Leu Asn Leu Gly
370 375

<210> 261

<211> 529

<212> PRT

<213> Helicobacter pylori

<400> 261

Met Lys Gln Asn Leu Lys Pro Phe Lys Met Ile Lys Glu Asn Leu Met
1 5 10 15

Thr Gln Ser Gln Lys Val Arg Phe Leu Ala Pro Leu Ser Leu Ala Leu
20 25 30

Ser Leu Ser Phe Asn Pro Val Gly Ala Glu Glu Asp Gly Gly Phe Met
35 40 45

Thr Phe Gly Tyr Glu Leu Gly Gln Val Val Gln Gln Val Lys Asn Pro
50 55 60

Gly Lys Ile Lys Ala Glu Glu Leu Ala Gly Leu Leu Asn Ser Asn Thr
65 70 75 80

Thr Asn Asn Thr Asn Thr Asn Ile Ala Gly Thr Gly Gly Asn Val Ala
85 90 95

Gly Thr Leu Gly Asn Leu Phe Met Asn Gln Leu Gly Asn Leu Ile Asp
100 105 110

Leu Tyr Pro Ile Leu Asn Thr Lys Asn Ile His Gln Cys Gly Thr Thr
115 120 125

Asn Asn Gly Ser Ser Ser Ala Thr Thr Ala Ala Ala Thr Thr Asn Asn
130 135 140

Gly Leu Cys Phe Gln Gly Asn Leu Asp Leu Tyr Asn Glu Met Val Gly
145 150 155 160

Ser Ile Lys Thr Leu Ser Gln Asn Ile Ser Lys Asn Ile Phe Gln Gly
165 170 175

Asn Asn Asn Thr Thr Ser Gln Asn Leu Ser Asn Gln Leu Ser Glu Leu
180 185 190

Asn Thr Ala Ser Val Tyr Leu Thr Tyr Met Asn Ser Phe Leu Asn Ala
195 200 205

Asn Asn Gln Ala Gly Gly Ile Phe Gln Asn Asn Thr Asn Gln Ala Tyr
210 215 220

Gly Asn Gly Val Thr Ala Gln Gln Ile Ala Tyr Ile Leu Lys Gln Ala
225 230 235 240

Ser Ile Thr Met Gly Pro Ser Gly Asp Ser Gly Ala Ala Ala Ala Phe
245 250 255

Leu Asp Ala Ala Leu Ala Gln His Val Phe Asn Ser Ala Asn Ala Gly
260 265 270

Asn Asp Leu Ser Ala Lys Glu Phe Thr Ser Leu Val Gln Asn Ile Val
275 280 285

Asn Asn Ser Gln Asn Ala Leu Thr Leu Ala Asn Asn Ala Asn Ile Ser
290 295 300

Asn Ser Thr Gly Tyr Gln Val Ser Tyr Gly Gly His Ile Asp Gln Ala
305 310 315 320

Arg Ser Thr Gln Leu Leu Asn Asn Thr Thr Asn Thr Leu Ala Lys Val
325 330 335

Thr Ala Leu Asn Asn Glu Leu Lys Ala Asn Pro Trp Leu Gly Asn Phe
340 345 350

Ala Ala Gly Asn Ser Ser Gln Val Asn Ala Phe Asn Gly Phe Ile Thr
355 360 365

Lys Ile Gly Tyr Lys Gln Phe Phe Gly Glu Asn Lys Asn Val Gly Leu
370 375 380

Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Gly Val Gly Asn Gly
385 390 395 400

Pro Thr Tyr Asn Gln Val Asn Leu Leu Thr Tyr Gly Val Gly Thr Asp
405 410 415

Val Leu Tyr Asn Val Phe Ser Arg Ser Phe Gly Ser Arg Ser Leu Asn
420 425 430

Ala Gly Phe Phe Gly Gly Ile Gln Leu Ala Gly Asp Thr Tyr Ile Ser
435 440 445

Thr Leu Arg Asn Ser Pro Gln Leu Ala Asn Arg Pro Thr Ala Thr Lys
450 455 460

Phe Gln Phe Leu Phe Asp Val Gly Leu Arg Met Asn Phe Gly Ile Leu
465 470 475 480

Lys Lys Asp Leu Lys Ser His Asn Gln His Ser Ile Glu Ile Gly Val
485 490 495

Gln Ile Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys Ala Gly Gly Ala Glu
500 505 510

Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp Val Tyr Gly Tyr Ala
515 520 525

Phe

<210> 262

<211> 2529

<212> PRT

<213> Helicobacter pylori

<400> 262

Met Ala Phe Lys Lys Ala Arg Leu Ile Ser Lys Phe Ile Ser Lys Gly
1 5 10 15

Ser Phe Lys Leu Asn Lys Ile Ser Lys Lys Ile Phe Thr Leu Asn Gln
20 25 30

Ile Leu Lys Cys Glu Lys Pro Leu Lys Arg His Lys Lys Ala Leu Lys
35 40 45

Pro Ile Lys Lys Leu Ser Asn Arg Asn Lys Ser Phe Leu Lys Ala Ser
50 55 60

Val Leu Leu Ile Gly Ala Leu Gly Gly Leu Ser His Leu Arg Ala Asn
65 70 75 80

Glu Cys Arg Tyr Trp Ser Trp Ser Ser Trp Ser Tyr Gln Asp Asn Ile
85 90 95

Glu Ser Gly Pro Asn Ser Pro Thr His Asn Ser Tyr Cys Leu Phe Ser
100 105 110

Ser Thr Gln Gly Ser Gly Thr Tyr Tyr Leu Asn Thr Leu Thr Thr Tyr
115 120 125

Ser Ala Gly Gly Ala Ser Phe Thr Gln Lys Phe Asn Asn Gly Thr Leu
130 135 140

Asn Val Gly Glu Asn Ile Arg Phe Gly Gly Thr Gly Ile Asn Gly Gly
145 150 155 160

Asp Val Gly Tyr Ile Thr Gly Thr Tyr Asp Ala Gln Thr Ile Asn Phe
165 170 175

Asn Ser Ser His Leu Thr Thr Gly Asn Ser Tyr Ala Asp Gly Gly Gly
180 185 190

Ala Thr Leu Asn Phe Asn Ala Ala Asn Asn Ile Thr Ile Asn Gln Ala
195 200 205

Ser Phe Asp Asn Ser His Ala Gly Thr Gln Lys Ser Tyr Met Asn Phe
210 215 220

Lys Gly Ser Asn Ile Lys Val Ser Gly Ser Ser Phe Thr Asp Asp Thr
225 230 235 240

Asp Gly Gly Phe Ser Phe Ser Gly Asn Ser Asn Asn Ser Thr Ile Ser
245 250 255

Phe Asn Gln Thr Ser Phe Asn Gln Gly Thr Tyr His Phe Ser Asn Ser
260 265 270

Ala Thr Leu Ser Phe Asn His Ser Ala Phe Asn Gln Gly Thr Tyr Asn
275 280 285

Phe Asn Ser Thr Gln Ser Ala Phe Asn Asn Ser Ala Phe Asn Gln Gly
290 295 300

Thr Tyr His Phe Asn Gly Asn Ala Ser Phe Asp Asn Asp Thr Phe Asn
305 310 315 320

Gln Gly Thr Tyr Ser Phe Asn Thr Ser Lys Val Ser Phe Ser Gly Ile
325 330 335

Asn Thr Leu Asn Ser Ser Ser Pro Phe Ala Ser Leu Lys Gly Ser Val
340 345 350

Ser Phe Gly Ser Asp Ala Ile Phe Asn Leu Asn Gln Thr Leu Asn Asn
355 360 365

Gln Thr Tyr Asp Ile Leu Thr Thr Asn Gly Ala Ile Gln Tyr Gly Val
370 375 380

Tyr Gln Ser Tyr Leu Trp Asp Leu Ile Asn Tyr Lys Gly Asp Lys Ala
385 390 395 400

Ile Ser His Val Glu Val Gly Asn Asn Thr Tyr Asp Val Thr Phe Asp
405 410 415

Ile Asn Gly Gln Asp Glu Thr Leu Gln Glu Thr Phe Asn Lys Gln Ser
420 425 430

Ile Ile Thr Gln Phe Leu Gly Asp Asp Leu Gln Gln Gln Ala Gln Lys
435 440 445

Thr Tyr Gln Gln Asp Leu Ser Asn Ser Gln Ser Ala Leu Asn Asn Ala
450 455 460

Ala Ser Asp Asn Lys Ile Ala Asn Ser Asp Thr Asp Tyr Thr Lys Asn
465 470 475 480

Lys Asn Ala Thr Ile Lys Lys Asp Ala Gln Gly Leu Glu Asn Thr Asn
485 490 495

Gln Gln Ile Ala Gln Asp Glu Gln Ala Leu Gln Gly Asp Leu Asp Lys
500 505 510

Leu Lys Gln Leu Ala Asn Ser Pro Thr Gly Phe Ser Glu Gln Ala Phe
515 520 525

Asn Gln Ala Gln Lys Gln Glu Gln Gln Asp Glu Gln Thr Leu Gln Asn
530 535 540

Glu Glu Lys Thr Phe Asn Ser Glu Gln Glu Gly Leu Lys Gln Ala Ile
545 550 555 560

Gln Gln Ala Gln Ala Gln Gln Gln Lys Gln Gln Gln Lys Gln Glu Gln
565 570 575

Gln Gln Ala Gln Gln Thr Tyr Gln Glu Asp Leu Thr His Ser Gln Ser
580 585 590

Ala Leu Asn Asp Val Ala Ser Asp Asn Thr Ile Ala Ser Asn Asp Thr
595 600 605

Asn Tyr Thr Asn Asn Gln Asn Thr Ala Ile Lys Glu Asp Ala Gln Gly
610 615 620

Leu Glu Asn Thr Asn Gln Gln Ile Ala Gln Asp Glu Gln Ala Leu Gln
625 630 635 640

Gly Asp Leu Asp Lys Leu Lys Gln Leu Ala Asn Ser Pro Thr Gly Phe
645 650 655

Ser Glu Gln Ala Phe Asn Gln Ala Gln Lys Gln Glu Gln Gln Asp Glu
660 665 670

Gln Thr Leu Gln Asn Glu Glu Lys Thr Phe Asn Ser Glu Gln Glu Arg
675 680 685

Leu Lys Gln Ala Ile Ala Asn Ala Lys Pro Thr Ser Pro Thr Pro Ser
690 695 700

His Ala Pro Thr Pro Thr Lys His Thr Ala Pro Asn Thr Pro Pro Asn
705 710 715 720

Lys Val Pro Pro Thr Pro Pro Thr Gln Asn Pro Pro Ala Glu Ser Val
725 730 735

Trp Ser Gly Val Tyr Trp Leu Gln Asn Lys Thr Tyr Ser Asn Lys Gly
740 745 750

Ile Tyr Tyr Ile Asp Pro Asn Leu Ser Gly Gln Ser Gly Gln Ser Gly
755 760 765

Asn Thr Leu Ser Thr Tyr Thr Ala Asn Leu Phe Gly Arg Ser Phe Ser
770 775 780

Val Asn Ile Gln Asn Gly Thr Leu Ile Ile Gly Asn Asn Thr Glu Ser
785 790 795 800

Val Asn Ser Asn Gly Leu Ile Trp Ile Gly His Gly Gly Phe Gly Tyr
805 810 815

Ile Thr Gly Thr Phe Ser Ala Ala Asn Ile Tyr Leu Thr Asn Asn Phe
820 825 830

Lys Thr Gly Glu Gly Val Ser Asn Ser Asp Gly Gly Gly Ala Asn Ile
835 840 845

Thr Phe Lys Ala Ser Asp Asn Ile Thr Met Asp Gly Leu Asn Tyr Asn
850 855 860

Asp Ala Glu Thr Val Thr Lys Met Ile Gln Thr Gly Ala Ser Gln His
865 870 875 880

Ser Tyr Ala Thr Phe Asp Ala Leu Asn Asn Ile Ser Val Thr Asn Ser
885 890 895

Ser Phe Ser Asp Met Thr Trp Gly Lys Phe Ser Phe Ser Ala Lys Asn
900 905 910

Ile Ser Phe Ser Asn Ala Ser Phe Ser Gly Phe Thr Asn Pro Gly Gly
915 920 925

Ser Ser Val Ile Ser Ala Asn Ala Thr Asn Ser Leu Ser Phe Ile Asn
930 935 940

Ser Arg Leu Asn Gly Gly Ala Val Tyr Asn Leu Gln Ala Asn Ser Leu
945 950 955 960

Ile Phe Asn Asn Thr Gln Ala Val Phe Asn Val Leu Tyr Ser Arg Gly
965 970 975

Thr Ser Asn Phe Asn Ala Thr Thr Gln Leu Leu Gly Asn Thr Asn Phe
980 985 990

Thr Leu Ser Ser Gln Ser Leu Leu Asn Phe Asn Gly Asp Thr Thr Leu
995 1000 1005

Gln Asn Asn Ala Asn Ile Thr Leu Gly Asn Lys Ser Gln Ala Ala
1010 1015 1020

Phe Lys Asn Ser Leu Thr Leu Asp Asn Asn Ser Asn Leu Ser Leu
1025 1030 1035

Asp Asn Gln Ser Val Leu Asn Ala Asn Asn Thr Ser Ala Phe Asn
1040 1045 1050

Asn Gln Ala Ser Leu Asn Ile Tyr Asn Gly Ser Gln Ala Thr Phe
1055 1060 1065

Asn Ser Leu Phe Phe Asn Gly Gly Thr Leu Ser Leu Asn Ala Ser
1070 1075 1080

Ser Lys Leu Asn Ala Ser Asn Ala Ser Phe Ser Asn Asn Thr Thr
1085 1090 1095

Ile Asn Leu Asp Asp Ser Val Leu Ser Ala Ser Asn Thr Ser Ser
1100 1105 1110

Leu Asn Ala Asn Ile Asn Phe Gln Gly Ala Ser Gln Ala Asp Phe
1115 1120 1125

Gly Gly Asn Thr Ile Ile Asp Thr Ala Ser Phe Asn Phe Asp Ser
1130 1135 1140

Ala Ser Ser Leu Asn Phe Asn Asn Leu Thr Ala Asn Gly Ala Leu
1145 1150 1155

Asn Phe Asn Gly Tyr Thr Pro Ser Leu Thr Lys Ala Leu Met Ser
1160 1165 1170

Val Ser Gly Gln Phe Val Leu Gly Asn Asn Gly Asp Ile Asn Leu
1175 1180 1185

Ser Asp Ile Asn Ile Phe Asp Asn Ile Thr Lys Ser Val Thr Tyr
1190 1195 1200

Asn Ile Leu Asn Ala Gln Lys Gly Ile Thr Gly Ile Ser Gly Ala
1205 1210 1215

Asn Gly Tyr Glu Lys Ile Leu Phe Tyr Gly Met Lys Ile Gln Asn
1220 1225 1230

Ala Thr Tyr Ser Asp Asn Asn Asn Ile Gln Thr Trp Ser Phe Ile
1235 1240 1245

Asn Pro Leu Asn Ser Ser Gln Ile Ile Gln Glu Ser Ile Lys Asn
1250 1255 1260

Gly Asp Leu Thr Ile Glu Val Leu Asn Asn Pro Asn Ser Ala Ser
1265 1270 1275

Asn Thr Ile Phe Asn Ile Ala Pro Glu Leu Tyr Asn Tyr Gln Ala
1280 1285 1290

Ser Lys Gln Asn Pro Thr Gly Tyr Ser Tyr Asp Tyr Ser Asp Asn
1295 1300 1305

Gln Ala Gly Thr Tyr Tyr Leu Thr Ser Asn Ile Lys Gly Leu Phe
1310 1315 1320

Thr Pro Lys Gly Ser Gln Thr Pro Gln Ala Pro Gly Thr Tyr Ser
1325 1330 1335

Pro Phe Asn Gln Pro Leu Ser Ser Leu Asn Ile Tyr Asn Lys Gly
1340 1345 1350

Phe Ser Ser Glu Asn Leu Lys Thr Leu Leu Gly Ile Leu Ser Gln
1355 1360 1365

Asn Ser Ala Thr Leu Lys Glu Met Ile Glu Ser Asn Gln Leu Asp
1370 1375 1380

Asn Ile Thr Asn Ile Asn Glu Val Leu Gln Leu Leu Asp Lys Ile
1385 1390 1395

Lys Ile Thr Gln Val Gln Lys Gln Ala Leu Leu Glu Thr Ile Asn
1400 1405 1410

His Leu Thr Asp Asn Ile Asn Gln Thr Phe Asn Asn Gly Asn Leu
1415 1420 1425

Ile Ile Gly Ala Thr Gln Asp Asn Val Thr Asn Ser Thr Ser Ser
1430 1435 1440

Ile Trp Phe Gly Gly Asn Gly Tyr Ser Ser Pro Cys Thr Leu Asp
1445 1450 1455

Ser Ala Thr Cys Ser Ser Phe Arg Asn Thr Tyr Leu Gly Gln Leu
1460 1465 1470

Leu Gly Ser Thr Ser Pro Tyr Leu Gly Tyr Ile Asn Ala Asp Phe
1475 1480 1485

Lys Ala Lys Ser Ile Tyr Ile Thr Gly Thr Ile Gly Ser Gly Asn
1490 1495 1500

Ala Phe Glu Ser Gly Gly Ser Ala Asp Val Thr Phe Gln Ser Ala
1505 1510 1515

Asn Asn Leu Val Leu Asn Lys Ala Asn Ile Glu Ala Gln Ala Thr
1520 1525 1530

Asp Asn Ile Phe Asn Leu Leu Gly Gln Lys Gly Ile Glu Lys Ile
1535 1540 1545

Phe Asn Gln Gly Asn Leu Ala Asn Val Leu Ser Gln Val Ala Met
1550 1555 1560

Glu Lys Ile Lys Gln Ala Gly Gly Leu Gly Asn Phe Ile Glu Asn
1565 1570 1575

Ala Leu Ser Pro Leu Ser Lys Glu Leu Pro Ala Ser Leu Gln Asn
1580 1585 1590

Glu Thr Leu Gly Gln Leu Ile Gly Gln Asn Asn Leu Asp Asp Leu
1595 1600 1605

Leu Asn Asn Ser Gly Val Met Asn Ala Ile Gln Asn Ile Ile Ser
1610 1615 1620

Lys Lys Leu Ser Ile Phe Gly Asn Phe Val Thr Pro Ser Ile Ile
1625 1630 1635

Glu Asn Tyr Leu Ala Lys Gln Ser Leu Lys Ser Met Leu Asp Asp
1640 1645 1650

Lys Gly Leu Leu Asn Phe Ile Gly Gly Tyr Met Asn Ala Ser Glu
1655 1660 1665

Leu Ser Ser Ile Leu Ser Val Val Leu Lys Asp Ile Thr Asn Pro
1670 1675 1680

Pro Thr Ser Leu Gln Lys Asp Ile Gly Val Val Ala Asn Asp Leu
1685 1690 1695

Leu Asn Glu Phe Leu Gly Gln Asp Val Ile Lys Lys Leu Glu Ser
1700 1705 1710

Gln Gly Leu Val Ser Asn Ile Ile Asn Asn Ile Ile Ser Gln Gly
1715 1720 1725

Gly Leu Ser Gly Val Tyr Asn Gln Gly Leu Gly Ser Val Leu Pro
1730 1735 1740

Pro Ser Leu Gln Asn Ala Leu Lys Glu Asn Asp Leu Gly Thr Leu
1745 1750 1755

Leu Ser Pro Arg Gly Leu His Asp Phe Trp Gln Lys Gly Tyr Phe
1760 1765 1770

Asn Phe Leu Ser Asn Gly Tyr Val Phe Val Asn Asn Ser Ser Phe
1775 1780 1785

Ser Asn Ala Thr Gly Gly Ser Leu Asn Phe Val Ala Asn Lys Ser
1790 1795 1800

Ile Ile Phe Asn Gly Asp Asn Thr Ile Asp Phe Ser Lys Tyr Gln
1805 1810 1815

Gly Ala Leu Ile Phe Ala Ser Asn Asp Val Ser Asn Ile Asn Ile
1820 1825 1830

Thr Thr Leu Asn Ala Thr Asn Gly Leu Ser Leu Asn Ala Gly Leu
1835 1840 1845

Asn Asn Val Ser Val Gln Lys Gly Glu Ile Cys Val Asn Leu Ala
1850 1855 1860

Asn Cys Pro Thr Thr Lys Asn Ser Ser Ser Thr Asn Ser Ser Val
1865 1870 1875

Thr Pro Thr Asn Glu Ser Leu Ser Val Arg Ala Asn Asn Phe Thr
1880 1885 1890

Phe Leu Gly Ala Ile Ala Ser Asn Gly Ala Ile Asp Leu Ser Gln
1895 1900 1905

Val Lys Asn Asn Ser Val Ile Asp Thr Leu Asn Leu Asn Glu Asn
1910 1915 1920

Ala Ala Leu Gln Ala Asn Asn Leu Thr Ile Thr Asn Ala Phe Asn
1925 1930 1935

Asn Ala Ser Asn Ser Thr Ala Asn Ile Asn Gly Asn Phe Thr Leu
1940 1945 1950

Asn Gln Gln Ala Thr Leu Ser Thr Asn Ala Ser Gly Leu Asn Val
1955 1960 1965

Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val Phe Asn Leu Ser
1970 1975 1980

His Ser Val Ser His Ala Ile Ile Asn Ala Gln Gly Ser Ala Thr
1985 1990 1995

Ile Met Ala Asn Asn Asn Asn Pro Leu Ile Gln Phe Asn Thr Ser
2000 2005 2010

Ser Lys Glu Val Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala
2015 2020 2025

Ile Tyr Tyr Gly Tyr Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu
2030 2035 2040

Asp Asn Tyr Leu Lys Leu Tyr Thr Leu Ile Asp Ile Asn Gly Lys
2045 2050 2055

His Met Val Met Thr Asp Asn Gly Leu Thr Tyr Asn Gly Gln Ala
2060 2065 2070

Val Ser Val Lys Asp Gly Gly Leu Val Val Gly Phe Lys Asp Ser
2075 2080 2085

Gln Asn Gln Tyr Ile Tyr Thr Ser Ile Leu Tyr Asn Lys Val Lys
2090 2095 2100

Ile Ala Val Ser Asn Asp Pro Ile Asn Asn Leu Gln Ala Pro Thr
2105 2110 2115

Leu Lys Gln Tyr Ile Ala Gln Ile Gln Gly Thr Gln Gly Val Asp
2120 2125 2130

Ser Ile Asp Gln Ala Gly Gly Ser Gln Ala Ile Asn Trp Leu Asn
2135 2140 2145

Lys Ile Phe Glu Thr Lys Gly Ser Pro Leu Phe Ala Pro Tyr Tyr
2150 2155 2160

Leu Glu Ser His Ser Thr Lys Asp Leu Thr Thr Ile Ala Gly Asp
2165 2170 2175

Ile Ala Asn Thr Leu Glu Val Ile Ala Asn Pro Asn Phe Lys Asn
2180 2185 2190

Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr Thr Gln Gln Met
2195 2200 2205

Ser Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe Ala Ser Ala
2210 2215 2220

Asp Phe His Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg Phe Ala
2225 2230 2235

Asp Ala Ile Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln
2240 2245 2250

Arg Asn Arg Val Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly
2255 2260 2265

Ala Ser Phe Ile Asn Gly Gly Thr Gly Thr Leu Tyr Gly Ile Asn
2270 2275 2280

Val Gly Tyr Asp Arg Phe Ile Lys Gly Val Ile Val Gly Gly Tyr
2285 2290 2295

Ala Ala Tyr Gly Tyr Ser Gly Phe His Ala Asn Ile Thr Gln Ser
2300 2305 2310

Gly Ser Ser Asn Val Asn Met Gly Val Tyr Ser Arg Ala Phe Ile
2315 2320 2325

Lys Arg Ser Glu Leu Thr Met Ser Leu Asn Glu Thr Trp Gly Tyr
2330 2335 2340

Asn Lys Thr Phe Ile Asn Ser Tyr Asp Pro Leu Leu Ser Ile Ile
2345 2350 2355

Asn Gln Ser Tyr Lys Tyr Asp Thr Trp Thr Thr Asp Ala Lys Ile
2360 2365 2370

Asn Tyr Gly Tyr Asp Phe Met Phe Lys Asp Lys Ser Val Ile Phe
2375 2380 2385

Lys Pro Gln Ile Gly Leu Ala Tyr Tyr Tyr Ile Gly Leu Ser Gly
2390 2395 2400

Leu Arg Gly Ile Met Asp Asp Pro Ile Tyr Asn Gln Phe Arg Ala
2405 2410 2415

Asn Ala Asp Pro Asn Lys Lys Ser Val Leu Thr Ile Asn Phe Ala
2420 2425 2430

Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser Tyr Tyr Phe Val
2435 2440 2445

Ile Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser Met Gly Asp
2450 2455 2460

Lys Met Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr Arg Asp
2465 2470 2475

Gly Gly Arg Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly Glu
2480 2485 2490

Ile Arg Leu Phe Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala
2495 2500 2505

Arg Phe Gly Leu Asp Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile
2510 2515 2520

Gly Met Arg Tyr Ala Phe
2525

<210> 263

<211> 193

<212> PRT

<213> Helicobacter pylori

<400> 263

Met Asn Thr Tyr Lys Asn Ser Leu Asn His Phe Leu Asn Leu Val Asp
1 5 10 15

Cys Leu Glu Lys Ile Pro Asn Val Gly Lys Lys Ser Ala Phe Lys Met
20 25 30

Ala Tyr His Leu Gly Leu Glu Asn Pro Tyr Leu Ala Leu Lys Ile Thr
35 40 45

His Ala Leu Glu Asn Ala Leu Glu Asn Leu Lys Thr Cys Ser Ser Cys
50 55 60

Asn Ala Leu Ser Glu Ser Glu Val Cys Glu Ile Cys Ser Asp Glu Ser
65 70 75 80

Arg Gln Asn Ser Gln Leu Cys Met Val Leu His Pro Arg Asp Val Phe
85 90 95

Ile Leu Glu Asp Leu Lys Asp Phe Leu Gly Arg Tyr Tyr Val Leu Asn
100 105 110

Ser Ile Glu Glu Val Asp Phe Asn Ala Leu Glu Lys Arg Leu Ile Glu
115 120 125

Glu Asn Ile Lys Glu Ile Ile Phe Ala Phe Pro Pro Thr Leu Ala Asn
130 135 140

Asp Ser Leu Met Leu Tyr Ile Glu Asp Lys Leu Gln His Phe His Leu
145 150 155 160

Thr Phe Thr Lys Ile Ala Gln Gly Val Pro Thr Gly Val Asn Phe Glu
165 170 175

Asn Ile Asp Ser Val Ser Leu Ser Arg Ala Phe Asn Ser Arg Ile Lys
180 185 190

Ala

<210> 264

<211> 188

<212> PRT

<213> Helicobacter pylori

<400> 264

Leu Phe Lys Arg Met Val Leu Ile Ala Leu Leu Gly Val Phe Ser Ser
1 5 10 15

Val Ser Leu Ser Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile Leu Val
20 25 30

Ser Asp Leu Lys Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp
35 40 45

Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val Ala Tyr
50 55 60

Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn
65 70 75 80

Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met Lys Tyr
85 90 95

Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr Thr Thr
100 105 110

Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile Gln Val
115 120 125

Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val Lys Ile
130 135 140

Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu Lys Ala
145 150 155 160

Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala Lys Val
165 170 175

Ala Gln Lys Glu Phe Gly Ser Val Cys Ala Leu Arg
180 185

<210> 265

<211> 353

<212> PRT

<213> Helicobacter pylori

<400> 265

Leu Lys His Leu Thr Pro Leu Thr His Thr Ile Phe Lys Ala Leu Trp
1 5 10 15

Leu Gly Thr Ala Leu Ser Ala Ser Leu Ser Leu Ala Ala Thr Glu Ser
20 25 30

Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro
35 40 45

Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Ile Lys
50 55 60

Asp Phe Asn Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe
65 70 75 80

Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys
85 90 95

Glu Ser Cys Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala
100 105 110

Gly Val Tyr His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His
115 120 125

Asn Asp Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys
130 135 140

Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp
145 150 155 160

Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn
165 170 175

Lys Gly Ser Arg Trp Glu Arg Ser Glu Lys Ser Asn Ala Asp Ala Glu
180 185 190

Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser
195 200 205

Lys Ile Phe Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser
210 215 220

Ala Asn Ser Asn Leu Asp Leu Asp Pro Ile Gly Asn Ala Met Pro Gln
225 230 235 240

Ala Leu Ile Ala Lys Glu Thr Lys Ile Glu Glu Thr Gln Ala Glu Lys
245 250 255

Ser Gln Glu Met Lys Glu Thr Thr Ser Glu Gln Thr Lys Ser Lys Pro
260 265 270

Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala Gln Ile Asn Ser Thr
275 280 285

Asp Phe Thr Pro Val Lys Lys Ser Pro Lys Lys Pro Ala Lys Val Ser
290 295 300

Gln Lys His Ser Phe Lys Asn Asn Ile Lys Asn Asn Val Lys Asn Asn
305 310 315 320

Ala Lys Thr Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro
325 330 335

Gly Gln Arg Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu
340 345 350

Leu

<210> 266

<211> 487

<212> PRT

<213> Helicobacter pylori

<400> 266

Met Ile Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile
1   5   10   15

Trp Ile Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly
            20   25   30

Gln Tyr Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln
        35   40   45

Ile Lys Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys
    50   55   60

Asp Ala Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Lys Asp
65   70   75   80

Gln Ile Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile
                85   90   95

Asn Gln Ala Leu Leu Arg Asn Leu Ala Leu Asp Leu Gly Leu Gly Ala
            100   105   110

Thr Lys Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Ser Val Phe Gln
        115   120   125

Lys Asp Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln
    130   135   140

Ser His Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu
145   150   155   160

Ile Leu Gln Lys Ile Ser Thr Leu Phe Pro Lys Thr Thr Thr Pro Leu
                165   170   175

Glu Gln Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp
            180   185   190

Ile Leu Ile Leu Asn Pro Ser Asp Val Lys Ile Ser Leu Asn Glu Glu
        195   200   205

Glu Met Lys Lys Tyr Tyr Glu Ser His Lys Lys Asp Phe Lys Lys Pro
    210   215   220

Thr Ser Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys
225   230   235   240

Pro Asp Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser
                245   250   255

Tyr Leu Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu
            260   265   270

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Gln Val Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu
        275                 280                 285

Arg Ser Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr
    290                 295                 300

Gln Asp Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln
305                 310                 315                 320

Lys Leu Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe
                325                 330                 335

Lys Asp Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu
            340                 345                 350

Leu Gln Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr
        355                 360                 365

Gln Glu Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu
    370                 375                 380

Lys Asp Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly
385                 390                 395                 400

Gly Thr Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn
                405                 410                 415

Ala Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn
            420                 425                 430

Lys Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe
        435                 440                 445

Ser Ala Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys
    450                 455                 460

Thr Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr
465                 470                 475                 480

Lys Ile Val Lys Tyr Ile Gln
                485
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<210> 267

<211> 443

<212> PRT

<213> Helicobacter pylori

<400> 267

Val Ser Pro Leu Lys Thr Ile Arg Ile Tyr Ser Tyr His Asp Ser Ile
1   5   10   15

Lys Asp Ser Ile Lys Ala Val Val Asn Ile Ser Thr Glu Lys Lys Ile
            20   25   30

Lys Asn Asn Phe Ile Gly Gly Gly Val Phe Asn Asp Pro Phe Phe Gln
        35   40   45

Gln Phe Phe Gly Asp Leu Gly Gly Met Ile Pro Lys Glu Arg Met Glu
    50   55   60

Arg Ala Leu Gly Ser Gly Val Ile Ile Ser Lys Asp Gly Tyr Ile Val
65   70   75   80

Thr Asn Asn His Val Ile Asp Gly Ala Asp Lys Ile Lys Val Thr Ile
                85   90   95

Pro Gly Ser Asn Lys Glu Tyr Ser Ala Thr Leu Val Gly Thr Asp Ser
            100   105   110

Glu Ser Asp Leu Ala Val Ile Arg Ile Thr Lys Asp Asn Leu Pro Thr
        115   120   125

Ile Lys Phe Ser Asp Ser Asn Asp Ile Ser Val Gly Asp Leu Val Phe
    130   135   140

Ala Ile Gly Asn Pro Phe Gly Val Gly Glu Ser Val Thr Gln Gly Ile
145   150   155   160

Val Ser Ala Leu Asn Lys Ser Gly Ile Gly Ile Asn Ser Tyr Glu Asn
                165   170   175

Phe Ile Gln Thr Asp Ala Ser Ile Asn Pro Gly Asn Ser Gly Gly Ala
            180   185   190

Leu Ile Asp Ser Arg Gly Gly Leu Val Gly Ile Asn Thr Ala Ile Ile
        195   200   205

Ser Lys Thr Gly Gly Asn His Gly Ile Gly Phe Ala Ile Pro Ser Asn
    210   215   220

Met Val Lys Asp Thr Val Thr Gln Leu Ile Lys Thr Gly Lys Ile Glu
225   230   235   240

Arg Gly Tyr Leu Gly Val Gly Leu Gln Asp Leu Ser Gly Asp Leu Gln
                245   250   255

Asn Ser Tyr Asp Asn Lys Glu Gly Ala Val Val Ile Ser Val Glu Lys
            260   265   270

Asp Ser Pro Ala Lys Lys Ala Gly Ile Leu Val Trp Asp Leu Ile Thr
275 280 285

Glu Val Asn Gly Lys Lys Val Lys Asn Thr Asn Glu Leu Arg Asn Leu
290 295 300

Ile Gly Ser Met Leu Pro Asn Gln Arg Val Thr Leu Lys Val Ile Arg
305 310 315 320

Asp Lys Lys Glu Arg Ala Phe Thr Leu Thr Leu Ala Glu Arg Lys Asn
325 330 335

Pro Asn Lys Lys Glu Thr Ile Ser Ala Gln Asn Gly Ala Gln Gly Gln
340 345 350

Leu Asn Gly Leu Gln Val Glu Asp Leu Thr Gln Glu Thr Lys Arg Ser
355 360 365

Met Arg Leu Ser Asp Asp Val Gln Gly Val Leu Val Ser Gln Val Asn
370 375 380

Glu Asn Ser Pro Ala Glu Gln Ala Gly Phe Arg Gln Gly Asn Ile Ile
385 390 395 400

Thr Lys Ile Glu Glu Val Glu Val Lys Ser Val Ala Asp Phe Asn His
405 410 415

Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg Phe Leu Val Leu Asp
420 425 430

Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys
435 440

<210> 268

<211> 288

<212> PRT

<213> Helicobacter pylori

<400> 268

Met Ser Lys Ser Leu Tyr Gln Thr Leu Asn Val Ser Glu Asn Ala Ser
1 5 10 15

Gln Asp Glu Ile Lys Lys Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His
20 25 30

Pro Asp Leu Asn Lys Thr Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile
35 40 45

Asn Ala Ala Tyr Glu Ile Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr
    50   55   60

Asp Gln Phe Gly Asp Asn Met Phe Gly Gly Gln Asn Phe Ser Asp Phe
65   70   75   80

Ala Arg Ser Arg Gly Pro Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser
                85   90   95

Ile Phe Gly Lys Gly Gly Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln
            100   105   110

Gly Phe Ser Gly Phe Asn Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp
        115   120   125

Ile Thr Ala Ala Leu Asn Val Ser Val Leu Asp Thr Leu Leu Gly Asn
    130   135   140

Lys Lys Gln Val Ser Ile Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro
145   150   155   160

Ile Gly Val Glu Glu Gly Glu Lys Ile Arg Val Arg Asn Lys Gly Lys
                165   170   175

Thr Gly Arg Thr Thr Arg Gly Asp Leu Leu Leu Glu Ile His Ile Glu
            180   185   190

Glu Asp Glu Met Tyr Arg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe
        195   200   205

Asp Leu Pro Leu Lys Thr Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala
    210   215   220

Thr Trp His Lys Thr Leu Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala
225   230   235   240

Met Gln Lys Phe Arg Ile Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr
                245   250   255

Ser His Val Gly Asp Leu Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys
            260   265   270

Thr Glu Thr Leu Ser Asn Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu
        275   280   285

<210> 269

<211> 295

<212> PRT

<213> Helicobacter pylori

<400> 269

Met Lys Gln Thr Thr Ile Asn His Ser Val Glu Leu Val Gly Ile Gly
1 5 10 15

Leu His Lys Gly Val Pro Val Lys Leu Val Leu Glu Pro Leu Gly Glu
20 25 30

Asn Gln Gly Ile Val Phe Tyr Arg Ser Asp Leu Gly Val Asn Leu Pro
35 40 45

Leu Lys Pro Glu Asn Ile Val Asp Thr Lys Met Ala Thr Val Leu Gly
50 55 60

Lys Asp Asn Ala Arg Ile Ser Thr Ile Glu His Leu Leu Ser Ala Val
65 70 75 80

His Ala Tyr Gly Ile Asp Asn Leu Lys Ile Ser Val Asp Asn Glu Glu
85 90 95

Ile Pro Ile Met Asp Gly Ser Ala Leu Thr Tyr Cys Met Leu Leu Asp
100 105 110

Glu Ala Gly Ile Lys Glu Leu Asp Ala Pro Lys Lys Val Met Glu Ile
115 120 125

Lys Gln Ala Val Glu Ile Arg Glu Ser Asp Lys Phe Val Lys Ile Glu
130 135 140

Pro Asp Ser Gln Leu Ser Leu Asn Phe Thr Ile Asp Phe Asn His Pro
145 150 155 160

Val Ile Ala Lys Gln Ala His His Phe Val Phe Ser Lys Thr Ala Tyr
165 170 175

Lys Glu Gln Val Ala Lys Ala Arg Thr Phe Gly Phe Leu Gln Glu Val
180 185 190

Asn Tyr Leu Arg Ser Ile Gly Leu Ala Lys Gly Gly Ser Leu Asn Asn
195 200 205

Cys Ile Val Leu Asp Glu Asn Ser Ile Leu Asn Lys Glu Gly Leu Arg
210 215 220

Cys Glu Lys Glu Phe Val Cys His Lys Ile Leu Asp Ala Met Gly Asp
225 230 235 240

Leu Met Val Leu Gly Met Pro Val Met Gly Lys Tyr Thr Ser Phe Ser
245 250 255

Gly Ser His Lys Leu Asn Ser Met Leu Val Lys Ala Ile Leu Ala Asp
260 265 270

Ala Lys Asn Tyr Glu Val Leu Ile Ala Ala Asp Pro Ala Lys Glu Phe
275 280 285

Ala Leu Gln Lys Ala Phe Ala
290 295

<210> 270

<211> 858

<212> PRT

<213> Helicobacter pylori

<400> 270

Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly
1 5 10 15

Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
20 25 30

Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys Lys Tyr
35 40 45

Phe Gly His Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
50 55 60

Phe Leu Leu Tyr Lys Thr Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
65 70 75 80

Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
85 90 95

Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
100 105 110

Leu Arg Pro Phe Ile Gly Asp Phe Gly Leu Tyr Ala Leu Ile Thr Leu
115 120 125

Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
130 135 140

Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Asn Leu Leu Lys Glu Ile
145 150 155 160

Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Pro Lys Lys
165 170 175

Glu Gly Phe Glu Asn Thr Pro Ser Asp Ile Gln Lys Lys Glu Thr Lys
180 185 190

Asn Asp Lys Glu Lys Glu Asn Arg Lys Glu Asn Pro Ile Asn Glu Asn
195 200 205

His Lys Thr Pro Asn Glu Glu Pro Phe Leu Ala Ile Pro Thr Pro Tyr
210 215 220

Asn Thr Thr Leu Asn Asp Ser Glu Pro Gln Glu Gly Leu Val Gln Ile
225 230 235 240

Ser Ser His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
245 250 255

Phe Asp Asp Leu Thr Asn Pro Thr Asn Pro Pro Leu Lys Glu Ile Lys
260 265 270

Gln Glu Thr Lys Glu Arg Glu Pro Thr Pro Thr Lys Glu Thr Leu Thr
275 280 285

Pro Thr Thr Pro Lys Pro Ile Met Pro Thr Leu Ala Pro Ile Ile Glu
290 295 300

Asn Asp Asn Lys Thr Glu Asn Gln Lys Thr Pro Asn His Pro Lys Lys
305 310 315 320

Glu Glu Asn Pro Gln Glu Asn Thr Gln Glu Glu Met Ile Glu Gly Arg
325 330 335

Ile Glu Glu Met Ile Lys Glu Asn Leu Lys Lys Glu Glu Lys Glu Val
340 345 350

Gln Asn Ala Pro Asn Phe Ser Pro Val Thr Pro Thr Ser Ala Lys Lys
355 360 365

Pro Val Met Val Lys Glu Leu Ser Glu Asn Lys Glu Ile Leu Asp Gly
370 375 380

Leu Asp Tyr Gly Glu Val Gln Lys Pro Lys Asp Tyr Glu Leu Pro Thr
385 390 395 400

Thr Gln Leu Leu Asn Ala Val Cys Leu Lys Asp Thr Ser Leu Asp Glu
405 410 415

Asn Glu Ile Asp Gln Lys Ile Gln Asp Leu Leu Ser Lys Leu Arg Thr
420 425 430

Phe Lys Ile Asp Gly Asp Ile Ile Arg Thr Tyr Ser Gly Pro Ile Val
435 440 445

Thr Thr Phe Glu Phe Arg Pro Ala Pro Asn Val Lys Val Ser Arg Ile
450 455 460

Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys Ala Glu Ser Ile
465 470 475 480

Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val Gly Ile Glu Ile
485 490 495

Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu Ile Leu Glu Ser
500 505 510

Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu Ala Leu Gly Lys
515 520 525

Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys Lys Leu Pro His
530 535 540

Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser Val Gly Val Asn
545 550 555 560

Ala Met Ile Leu Ser Leu Leu Tyr Lys Asn Pro Pro Asp Gln Leu Lys
565 570 575

Leu Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp
580 585 590

Ile Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys Ala Ile
595 600 605

Gly Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr Ser Leu
610 615 620

Met Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu Gln Ala
625 630 635 640

Pro Ser Asn Gly Val Glu Ala Phe Pro Tyr Leu Ile Val Val Ile Asp
645 650 655

Glu Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu Phe Pro
660 665 670

Ile Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His Leu Ile
675 680 685

Val Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys
690 695 700

Thr Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys Ile Asp
705 710 715 720

Ser Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu Gly Arg
725 730 735

Gly Asp Met Leu Phe Thr Pro Pro Gly Ala Asn Gly Leu Val Arg Leu
740 745 750

His Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val Asp Phe
755 760 765

Ile Lys Ala Gln Lys Glu Val Gln Tyr Asp Lys Asp Phe Leu Leu Glu
770 775 780

Glu Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile
785 790 795 800

Leu Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr
805 810 815

Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr
820 825 830

Ile Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala
835 840 845

Lys Gly Asn Arg Glu Ile Leu Gln Asn Phe
850 855

<210> 271

<211> 290

<212> PRT

<213> Helicobacter pylori

<400> 271

Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu Gly
1 5 10 15

Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu
20 25 30

Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln Ala
35 40 45

Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys
50 55 60

Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys Asn
65 70 75 80

Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn Tyr
85 90 95

Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly
100 105 110

Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys
115 120 125

Asp Leu Lys Tyr Ala Glu Gly Cys Ala Ser Leu Gly Gly Ile Tyr His
130 135 140

Asp Gly Lys Val Val Thr Arg Asp Phe Lys Lys Ala Val Glu Tyr Phe
145 150 155 160

Thr Lys Ala Cys Asp Leu Asn Asp Gly Asp Gly Cys Thr Ile Leu Gly
165 170 175

Ser Leu Tyr Asp Ala Gly Arg Gly Thr Pro Lys Asp Leu Lys Lys Ala
180 185 190

Leu Ala Ser Tyr Asp Lys Ala Cys Asp Leu Lys Asp Ser Pro Gly Cys
195 200 205

Phe Asn Ala Gly Asn Met Tyr His His Gly Glu Gly Ala Thr Lys Asn
210 215 220

Phe Lys Glu Ala Leu Ala Arg Tyr Ser Lys Ala Cys Glu Leu Glu Asn
225 230 235 240

Gly Gly Gly Cys Phe Asn Leu Gly Ala Met Gln Tyr Asn Gly Glu Gly
245 250 255

Val Thr Arg Asn Glu Lys Gln Ala Ile Glu Asn Phe Lys Lys Gly Cys
260 265 270

Lys Leu Gly Ala Lys Gly Ala Cys Asp Ile Leu Lys Gln Leu Lys Ile
275 280 285

Lys Val
290

<210> 272

<211> 957

<212> PRT

<213> Helicobacter pylori

<400> 272

Val Lys Leu Pro Lys Ala Leu Asn Glu Ala Thr Ala Gly Ala Ala Leu
1   5   10   15

Lys Tyr His Ile Lys Arg Ala Leu Glu Arg Ser His Ser Ile Ser Asp
            20   25   30

Phe Ser Lys Asn Leu Glu Leu Ser Thr Gln Lys Ser His Phe Ser Asn
        35   40   45

Asn Thr Leu Lys Ile Ile Glu Glu Leu Asn Asn Gly Val Lys Gln Ala
    50   55   60

Ser Glu Glu Ile Lys Glu Lys Ala Arg Asp Phe Ser Asn Gln Lys Leu
65   70   75   80

Thr Asn Glu Gln Ile Lys Asp Leu Leu Asn Asn Ala Glu Ile Pro Thr
                85   90   95

Ser Gly Arg Asp Ala Ile Thr Phe Gly Val Asn Asn Leu Asn Pro Glu
            100   105   110

Ile Val Glu Phe Leu His Lys Asn Asn Lys Lys Met Ile Ile Glu Lys
        115   120   125

Ala Ser Asn Lys Glu Leu Glu Leu Leu Lys Asp Ala Asn Phe Lys His
    130   135   140

Pro Glu Asn Ile Arg Ala Ser Leu Asp His Asp Ala Ile Ala His Ile
145   150   155   160

Leu Lys Arg His Gly Val Asn Ser Val Asn Val Arg Asn Gly Glu Ile
                165   170   175

Pro Ile Thr Asn Glu Asp Ile Ala Asn Tyr Arg Tyr Ile Val Asn Asn
            180   185   190

Ala Asp Ala Ile Leu Arg Thr Leu Asp Asn Glu Asn Lys Glu Leu Ile
        195   200   205

Ser Ala Phe Lys Gln Ile Asn Gly Tyr Ala Val Val Val Glu Gln Ala
    210   215   220

Ile Asn Lys Lys Asn Glu Leu Val Leu Lys Thr Met Tyr Lys Ser Lys
225   230   235   240

Gly Asp Tyr Lys Asp Asn Asn Ala Tyr Lys Lys Phe Ser Ser Thr His
                245   250   255

Thr Leu Asn Ala Asp Ala Lys Val Asn His Arg Leu Ser Ser Tyr Ser
            260   265   270

Gly Ala Thr Glu Asn Thr Thr Gln Lys Asp Leu Ile Asp Gln Glu Asn
275 280 285

Leu Leu Lys Thr Ser Glu Asn Leu Asn Glu Ser Thr Pro Lys Pro Thr
290 295 300

Asn Leu Ser Pro Leu Glu Gln Ala Asn Ala Glu Lys Leu Ala Lys Leu
305 310 315 320

Glu Ser Glu Lys Leu Glu Ser Glu Lys Glu Phe Leu Lys Ala Lys Glu
325 330 335

Gln Glu Ala Thr Arg Lys Ala Ala Leu Lys Lys Lys Leu Glu His Glu
340 345 350

Arg Gly Asn Ala Gly Asn Ile Glu Ser Gln Thr Lys Ile Glu Val Gly
355 360 365

Glu Asp Ile Pro Thr Gln Thr Gln Ala Gln Leu Pro Lys Ser Arg Val
370 375 380

Arg Leu Asn Glu Arg Glu Ile Tyr Asp Leu Asp Tyr Ala Ile Val Lys
385 390 395 400

Ala Lys Asp Leu Lys Pro Ser Phe Thr Thr Gly Gly Thr Gln Lys Arg
405 410 415

Thr Asp Met Asn Glu Glu Gln Ile Lys Ser Ile Ala Glu Asn Phe Asp
420 425 430

Pro Lys Lys Ile Phe Gly Ser Gly Gly Phe Glu Asp Leu Pro Ile Ile
435 440 445

Leu His Asp Gly Gln Val Ile Ala Gly Asn His Arg Ile Gln Gly Met
450 455 460

Leu Asn Phe Thr Pro Lys Ser Arg Phe Ser Tyr Glu Arg Ala Ile Lys
465 470 475 480

Glu Tyr Tyr His Ile Asp Leu Lys Pro Asp Glu Leu Leu Val Arg Val
485 490 495

Pro His Lys Arg Leu Asn Asn Thr Glu Ile Asn Asn Leu Ala Ala Ser
500 505 510

Ser Asn Gln Gly Arg Phe Asn Ser Glu Ser Asp His Ala Ile Ala Val
515 520 525

Leu Ser His Tyr Glu Ala Lys Leu Lys Glu Leu Asp Gln Lys Leu Asp
530 535 540

Ala Asp Ser Ile Tyr Ser Leu Lys Asn Ile Val Ala Lys Asn Leu Asn
545 550 555 560

Phe Asp Lys Ala Thr His Pro Asn Val Thr Asp Ser Asn Leu Ala Leu
565 570 575

Leu Met Phe Asn Met Pro Arg Thr Lys Thr Gln Gly Ile Glu Leu Leu
580 585 590

Asn Arg Trp Lys Lys Glu Phe Ser Asn Asp Ile Lys Ser Tyr Glu Lys
595 600 605

Val Lys Lys Met Phe Val Asp Asn Ala Gly Ser Phe His Asn Leu Ile
610 615 620

His Asp Leu Asn Phe Pro Lys Val Ser Leu Asn Ala Tyr Leu Ser Asp
625 630 635 640

Ile Met Asp Arg Ser Phe Ala Asn Leu Lys Asn Tyr Gln Ser Thr Ser
645 650 655

Glu Ser Leu Lys Asp Leu Ser Glu Lys Phe Tyr Lys Thr Ser Ser Leu
660 665 670

Glu Met Phe Glu Lys Ser Asp Gln Ser Thr Ser Asp Ile Ser Glu Ile
675 680 685

Leu Gly Gly Ala Ile Ala Arg Phe Ala Arg Phe Asp Asp Pro Ser Lys
690 695 700

Ala Leu Phe Glu Ala Leu Arg Ser Asp Asn Ile Lys Lys Gly Leu Lys
705 710 715 720

Asp Tyr Lys Ile Ala Asp Val Thr Lys Asp Met Phe Asn Ala Asp Ser
725 730 735

Lys Glu Phe Lys Asp Ile Asp Ile Tyr Asp Phe Thr His Tyr Leu Leu
740 745 750

Met Val Asn Arg Glu Pro Asn Glu Asn Asn Pro Ile Leu Lys Arg Leu
755 760 765

Ile Glu Ala Val Lys Asp Met Gln Lys Glu Ser Glu Lys Gly Ile Lys
770 775 780

Gln Lys Leu Glu Thr Pro Ser Glu Trp Gly His Asn Tyr Ser Glu Phe
785 790 795 800

Lys Gly Asp Gly Leu Gly Ala Ile Asn Lys Leu Leu Glu Thr Lys Lys
805 810 815

Gly Phe Val Ala Gly Ala Phe His Lys Glu Gly Leu Gly Asp Ile Asp
820 825 830

Leu Val Tyr Gly Asn Ser Lys Tyr Gly Leu Glu His Ile Phe Asn Arg
835 840 845

Arg Glu Ser Asp Ala Ile Asp Lys Gly Met Ser Lys Glu Glu Ala Lys
850 855 860

Lys Tyr Ala Leu Lys Ile Ile Asn Asn Ile Pro Asn Ile Ile Ser Asn
865 870 875 880

Gly Lys Leu Ser Lys Asp Asn Leu Gly Arg Leu Ser Ile Glu Phe Glu
885 890 895

Asn Gln Arg Val Gly Leu Asn Asp Ser Trp Lys Gly Glu Thr Leu Asn
900 905 910

Asn Arg Trp Val Ile Thr Ser Tyr Glu Ile Asp Lys Ser Arg Asn Gly
915 920 925

Leu Ile Glu Ser Pro Leu Ala Pro Asn Tyr Lys Gly Lys Asp Thr Asn
930 935 940

Pro Leu Asn Leu Asp Ser Pro Asn Pro Thr Thr Lys Asn
945 950 955

<210> 273

<211> 256

<212> PRT

<213> Helicobacter pylori

<400> 273

Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
1 5 10 15

Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn
20 25 30

Tyr Ile Tyr Lys Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg
35 40 45

Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala
50 55 60

Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys
65 70 75 80

Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp
85 90 95

Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg
100 105 110

Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala
115 120 125

Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr
130 135 140

Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys
145 150 155 160

Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu
165 170 175

Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp
180 185 190

Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser
195 200 205

Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly
210 215 220

Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys
225 230 235 240

Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg
245 250 255

<210> 274

<211> 606

<212> PRT

<213> Helicobacter pylori

<400> 274

Met Gly Gly Ile Leu Ser Ser Leu Asn Thr Ser Tyr Thr Gly Leu Gln
1 5 10 15

Ala His Gln Ser Met Val Asp Val Thr Gly Asn Asn Ile Ser Asn Ala
20 25 30

Ser Asp Glu Phe Tyr Ser Arg Gln Arg Val Ile Ala Lys Pro Gln Ala
35 40 45

Ala Tyr Met Tyr Gly Thr Lys Asn Val Asn Met Gly Val Asp Val Glu
    50   55   60

Ala Ile Glu Arg Val His Asp Glu Phe Val Phe Ala Arg Tyr Thr Lys
65   70   75   80

Ala Asn Tyr Glu Asn Thr Tyr Tyr Asp Thr Glu Phe Ser His Leu Lys
                85   90   95

Glu Ala Ser Ala Tyr Phe Pro Asp Ile Asp Glu Ala Ser Leu Phe Thr
            100   105   110

Asp Leu Gln Asp Tyr Phe Asn Ser Trp Lys Glu Leu Ser Lys Asn Ala
        115   120   125

Lys Asp Ser Ala Gln Lys Gln Ala Leu Ala Gln Lys Thr Glu Ala Leu
    130   135   140

Thr His Asn Ile Lys Asp Thr Arg Glu Arg Leu Thr Thr Leu Gln His
145   150   155   160

Lys Ala Ser Glu Glu Leu Lys Ser Val Ile Lys Glu Val Asn Ser Leu
                165   170   175

Gly Ser Gln Ile Ala Glu Ile Asn Lys Arg Ile Lys Glu Val Glu Asn
            180   185   190

Asn Lys Ser Leu Lys His Ala Asn Glu Leu Arg Asp Lys Arg Asp Glu
        195   200   205

Leu Glu Phe His Leu Arg Glu Leu Leu Gly Gly Asn Val Phe Lys Ser
    210   215   220

Ser Ile Lys Thr His Ser Leu Thr Asp Lys Asp Ser Ala Asp Phe Asp
225   230   235   240

Glu Ser Tyr Asn Leu Asn Ile Gly His Gly Phe Asn Ile Ile Asp Gly
                245   250   255

Ser Ile Phe His Pro Leu Val Val Lys Glu Ser Glu Asn Lys Gly Gly
            260   265   270

Leu Asn Gln Val Tyr Phe Gln Ser Asp Asp Phe Lys Val Thr Asn Ile
        275   280   285

Thr Asp Lys Leu Asn Gln Gly Arg Val Gly Ala Leu Leu Asn Val Tyr
    290   295   300

Asn Asp Gly Ser Asn Gly Thr Leu Lys Gly Lys Leu Gln Asp Tyr Ile
305   310   315   320

Asp Leu Leu Asp Ser Phe Ala Lys Gly Leu Ile Glu Ser Thr Asn Ala
325 330 335

Ile Tyr Ala Gln Ser Ala Ser His Tyr Ile Glu Gly Glu Pro Val Glu
340 345 350

Phe Asn Ser Asp Glu Ala Phe Lys Asp Thr Asn Tyr Asn Ile Lys Asn
355 360 365

Gly Ser Phe Asp Leu Ile Ala Tyr Asn Thr Asp Gly Lys Glu Ile Ala
370 375 380

Arg Lys Thr Ile Ala Ile Thr Pro Ile Thr Thr Met Asn Asp Ile Ile
385 390 395 400

Gln Ala Ile Asn Ala Asn Thr Asp Asp Asn Gln Asp Asn Asn Thr Glu
405 410 415

Asn Asp Phe Asp Asp Tyr Phe Thr Ala Gly Phe Asn Asn Glu Thr Lys
420 425 430

Lys Phe Val Ile Gln Pro Lys Asn Ala Ser Gln Gly Leu Phe Val Ser
435 440 445

Met Lys Asp Asn Gly Thr Asn Phe Met Gly Ala Leu Lys Leu Asn Pro
450 455 460

Phe Phe Gln Gly Asp Asp Ala Ser Asn Ile Ser Leu Asn Lys Glu Tyr
465 470 475 480

Lys Lys Glu Pro Thr Thr Ile Arg Pro Trp Leu Ala Pro Ile Asn Gly
485 490 495

Asn Phe Asp Val Ala Asn Met Met Gln Gln Leu Gln Tyr Asp Ser Val
500 505 510

Asp Phe Tyr Asn Asp Lys Phe Asp Ile Lys Pro Met Lys Ile Ser Glu
515 520 525

Phe Tyr Gln Phe Leu Thr Gly Lys Ile Asn Thr Asp Ala Glu Lys Ser
530 535 540

Gly Arg Ile Leu Asp Thr Lys Lys Ser Met Leu Glu Thr Ile Lys Lys
545 550 555 560

Glu Gln Leu Ser Ile Ser Gln Val Ser Val Asp Glu Glu Met Val Asn
565 570 575

Leu Ile Lys Phe Gln Ser Gly Tyr Ala Ala Asn Ala Lys Val Ile Thr
580 585 590

Ala Ile Asp Arg Met Ile Asp Thr Leu Leu Gly Ile Lys Gln
595 600 605

<210> 275

<211> 417

<212> PRT

<213> Helicobacter pylori

<400> 275

Met Arg Tyr Leu Trp Leu Phe Leu Ile His Thr Ile Gly Leu Phe Ala
1 5 10 15

Thr Asp Lys Thr Leu Asp Ile Ile Lys Thr Ile Gln Lys Leu Pro Lys
20 25 30

Ile Glu Val Arg Tyr Ser Ile Asp Asn Asp Ala Asn Tyr Ala Leu Lys
35 40 45

Leu His Glu Val Leu Ala Asn Asp Leu Lys Thr Ser Gln His Phe Asp
50 55 60

Val Ser Gln Asn Lys Asp Gln Gly Ala Ile Asn Tyr Ala Glu Leu Lys
65 70 75 80

Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala Val Glu Asn
85 90 95

Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp Thr Gly Thr
100 105 110

Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp Leu Tyr Pro
115 120 125

Phe Ala Ala His Asn Met Ala Ile Val Val Asn Asp Tyr Leu Lys Ala
130 135 140

Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser Lys Tyr Ile
145 150 155 160

Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asp Tyr Thr Met Arg Tyr
165 170 175

Gln Lys Glu Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe Pro Lys Trp
180 185 190

Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr Thr Gln Tyr Gly Glu Arg
195 200 205

Thr Pro Met Ile Leu Lys Tyr Asn Ile Gln Lys Ala Thr His Glu Asn
    210   215   220

Ile Ala Ser Ser Gln Gly Met Ala Val Val Ser Ser Val Ser Ser Asp
225   230   235   240

Gly Ser Lys Ile Leu Met Ser Leu Ala Pro Asp Gly Gln Pro Asp Val
                245   250   255

Tyr Leu Tyr Asp Thr His Lys Lys Thr Lys Thr Lys Ile Thr Arg Tyr
            260   265   270

Pro Gly Ile Asp Val Ser Gly Val Phe Leu Glu Asp Asp Lys Ser Met
        275   280   285

Ala Phe Val Ser Asp Arg Ser Gly Tyr Pro Asn Ile Tyr Met Lys Lys
    290   295   300

Leu Gly Leu Lys Glu Ser Ala Glu Gln Leu Leu Tyr Glu Gly Arg Ser
305   310   315   320

Asn Glu Ser Ile Asp Ala Tyr Lys Asp Ser Ile Val Tyr Val Ser Arg
                325   330   335

Glu Asn Leu Asn Glu Phe Gly Lys Thr Val Phe Asn Leu Asn Leu Ile
            340   345   350

Thr Leu Asn Ser Lys Tyr Ile Arg Arg Leu Thr Val Asn Gly Ser Asn
        355   360   365

Gln Met Pro Arg Phe Ser Thr Asp Gly Arg Asn Ile Met Tyr Ile Lys
    370   375   380

Lys Thr Pro Gln Glu Tyr Ala Met Gly Leu Ile Leu Leu Asp Tyr Asn
385   390   395   400

Gln Ser Phe Leu Phe Pro Leu Lys Asn Val Lys Ile Gln Ala Phe Asp
                405   410   415

Trp

<210> 276

<211> 448

<212> PRT

<213> Helicobacter pylori

<400> 276

Met Phe Gln Ala Leu Ser Asp Gly Phe Lys Asn Ala Leu Asn Lys Ile
1   5   10   15

Arg Phe Gln Asp Asp Glu Lys Ala Leu Asp Arg Ala Leu Asp Glu Leu
            20   25   30

Lys Lys Thr Leu Leu Lys Asn Asp Val His His Lys Val Ala Arg Glu
        35   40   45

Leu Leu Lys Lys Val Glu Ser Gln Thr Lys Leu Asn Gly Ile Gly Lys
    50   55   60

Gln Gln Phe Leu Asp Ala Leu Glu Lys Ser Leu Leu Glu Ile Leu Ser
65   70   75   80

Ala Lys Gly Ser Ser Gly Phe Thr Phe Ala Gln Thr Pro Pro Thr Val
                85   90   95

Val Leu Met Ala Gly Leu Gln Gly Ser Gly Lys Thr Thr Thr Thr Ala
            100   105   110

Lys Leu Ala His Tyr Leu Lys Thr Lys Asn Lys Lys Val Leu Leu Cys
        115   120   125

Ala Cys Asp Leu Gln Arg Leu Ala Ala Val Glu Gln Leu Lys Val Leu
    130   135   140

Gly Glu Gln Val Gly Val Glu Val Phe Tyr Glu Glu Asn Lys Ser Val
145   150   155   160

Lys Glu Ile Ala Ser Asn Ala Leu Lys Arg Ala Lys Glu Ala Gln Phe
                165   170   175

Asp Val Leu Leu Val Asp Ser Ala Gly Arg Leu Ala Ile Asp Lys Glu
            180   185   190

Leu Met Gln Glu Leu Lys Glu Val Lys Glu Ile Leu Asn Pro His Glu
        195   200   205

Val Leu Tyr Val Ala Asp Ala Leu Ser Gly Gln Asp Gly Val Lys Ser
    210   215   220

Ala Asn Thr Phe Asn Glu Glu Ile Gly Val Ser Gly Val Val Leu Ser
225   230   235   240

Lys Phe Asp Ser Asp Ser Lys Gly Gly Ile Ala Leu Gly Ile Thr Tyr
                245   250   255

Gln Leu Gly Leu Pro Leu Arg Phe Ile Gly Ser Gly Glu Lys Ile Pro
            260   265   270

Asp Leu Asp Val Phe Val Pro Glu Arg Ile Val Gly Arg Leu Met Gly
275 280 285

Ala Gly Asp Ile Val Ser Leu Ala Glu Lys Thr Ala Ser Val Leu Asn
290 295 300

Pro Asn Glu Ala Lys Asp Leu Ser Lys Lys Leu Lys Lys Gly Gln Phe
305 310 315 320

Thr Phe Asn Asp Phe Leu Asn Gln Ile Glu Lys Val Lys Lys Leu Gly
325 330 335

Ser Met Ser Ser Leu Ile Ser Met Ile Pro Gly Leu Gly Asn Met Ala
340 345 350

Ser Ala Leu Lys Asp Thr Asp Leu Glu Ser Ser Leu Glu Val Lys Lys
355 360 365

Ile Lys Ala Met Val Asn Ser Met Thr Lys Lys Glu Gln Glu Asn Pro
370 375 380

Glu Ile Leu Asn Gly Ser Arg Arg Lys Arg Ile Ala Leu Gly Ser Gly
385 390 395 400

Leu Glu Val Ser Glu Ile Asn Arg Ile Ile Lys Arg Phe Asp Gln Ala
405 410 415

Ser Lys Met Ala Lys Arg Leu Thr Asn Lys Lys Gly Ile Ser Asp Leu
420 425 430

Met Asn Leu Met Ser Gln Ala Lys Asn Gln Thr Pro Pro Lys Met Arg
435 440 445

<210> 277

<211> 874

<212> PRT

<213> Helicobacter pylori

<400> 277

Met Ile Met Lys Gln Glu Pro Thr Thr Tyr Gln Pro Glu Glu Ile Glu
1 5 10 15

Lys Lys Ile Tyr Glu Ile Cys Ser His Arg Gly Tyr Phe Glu Ile Asp
20 25 30

Gly Asn Glu Ala Ile Gln Glu Lys Asn Lys Arg Phe Cys Leu Met Met
35 40 45

```
Pro Pro Pro Asn Val Thr Gly Val Leu His Ile Gly His Ala Leu Thr
    50                  55                  60

Leu Ser Leu Gln Asp Ile Leu Ala Arg Tyr Lys Arg Met Asp Gly Tyr
65                  70                  75                  80

Lys Thr Leu Tyr Gln Pro Gly Leu Asp His Ala Gly Ile Ala Thr Gln
                85                  90                  95

Asn Val Val Glu Lys Gln Leu Leu Ser Gln Gly Ile Lys Lys Glu Asp
            100                 105                 110

Leu Gly Arg Glu Glu Phe Ile Lys Lys Val Trp Glu Trp Lys Glu Lys
        115                 120                 125

Ser Gly Gly Ala Ile Leu Glu Gln Met Lys Arg Leu Gly Val Ser Ala
    130                 135                 140

Ala Phe Ser Arg Thr Arg Phe Thr Met Asp Lys Gly Leu Gln Arg Ala
145                 150                 155                 160

Val Lys Leu Ala Phe Leu Lys Trp Tyr Glu Lys Gly Leu Ile Ile Gln
                165                 170                 175

Asp Asn Tyr Met Val Asn Trp Cys Thr Lys Asp Gly Ala Leu Ser Asp
            180                 185                 190

Ile Glu Val Glu Tyr Glu Glu Arg Lys Gly Ala Leu Tyr Tyr Ile Arg
        195                 200                 205

Tyr Tyr Leu Glu Asn Gln Lys Asp Tyr Leu Val Val Ala Thr Thr Arg
    210                 215                 220

Pro Glu Thr Leu Phe Gly Asp Ser Ala Leu Met Val Asn Pro Asn Asp
225                 230                 235                 240

Glu Arg Tyr Lys His Leu Val Gly Gln Lys Ala Ile Leu Pro Leu Ile
                245                 250                 255

His Arg Thr Ile Pro Ile Ile Ala Asp Glu His Val Glu Met Glu Phe
            260                 265                 270

Gly Thr Gly Cys Val Lys Val Thr Pro Gly His Asp Phe Asn Asp Tyr
        275                 280                 285

Glu Val Gly Lys Arg His His Leu Glu Thr Ile Lys Ile Phe Asp Glu
    290                 295                 300

Lys Gly Ile Leu Asn Ala His Cys Gly Glu Phe Glu Asn Leu Glu Arg
305                 310                 315                 320
```

Leu Glu Ala Arg Asp Lys Val Val Glu Arg Leu Lys Glu Asn Ala Leu
325 330 335

Leu Glu Lys Ile Glu Glu His Thr His Gln Val Gly His Cys Tyr Arg
340 345 350

Cys His Asn Val Val Glu Pro Tyr Val Ser Lys Gln Trp Phe Val Lys
355 360 365

Pro Glu Ile Ala Gln Ser Ser Ile Glu Lys Ile Gln Gln Gly Leu Ala
370 375 380

Arg Phe Tyr Pro Ser Asn Trp Ile Asn Asn Tyr Asn Ala Trp Met Arg
385 390 395 400

Glu Leu Arg Pro Trp Cys Ile Ser Arg Gln Leu Phe Trp Gly His Gln
405 410 415

Ile Pro Val Phe Thr Cys Glu Asn Asn His Gln Phe Val Ser Leu Asp
420 425 430

Thr Pro Leu Ser Cys Pro Thr Cys Lys Ser Glu Thr Leu Glu Gln Asp
435 440 445

Lys Asp Val Leu Asp Thr Trp Phe Ser Ser Gly Leu Trp Ala Phe Ser
450 455 460

Thr Leu Gly Trp Gly Gln Glu Lys Ser Gly Leu Phe Asn Glu Ser Asp
465 470 475 480

Leu Lys Asp Phe Tyr Pro Asn Thr Thr Leu Ile Thr Gly Phe Asp Ile
485 490 495

Leu Phe Phe Trp Val Ala Arg Met Leu Phe Cys Ser Glu Ser Leu Leu
500 505 510

Gly Glu Leu Pro Phe Lys Asp Ile Tyr Leu His Ala Leu Val Arg Asp
515 520 525

Glu Lys Gly Glu Lys Met Ser Lys Ser Lys Gly Asn Val Ile Asp Pro
530 535 540

Leu Glu Met Ile Glu Lys Tyr Gly Ala Asp Ser Leu Arg Phe Thr Leu
545 550 555 560

Ala Asn Leu Cys Ala Thr Gly Arg Asp Ile Lys Leu Ser Thr Thr His
565 570 575

Leu Glu Asn Asn Lys Asn Phe Ala Asn Lys Leu Phe Asn Ala Ala Ser
580 585 590

Tyr Leu Lys Leu Lys Gln Glu Ser Phe Lys Asp Lys Glu Arg Leu Asn
595 600 605

Glu Tyr Gln Thr Pro Leu Gly Arg Tyr Ala Lys Ser Arg Leu Asn Ser
610 615 620

Ala Thr Lys Glu Ala Arg Asn Ala Leu Asp Asn Tyr Arg Phe Asn Asp
625 630 635 640

Ala Thr Thr Leu Leu Tyr Arg Phe Leu Trp Gly Glu Phe Cys Asp Trp
645 650 655

Phe Ile Glu Phe Ser Lys Val Glu Asn Glu Ala Ile Asp Glu Leu Gly
660 665 670

Ser Val Leu Lys Glu Ala Leu Lys Leu Leu His Pro Phe Met Pro Phe
675 680 685

Ile Ser Glu Ser Leu Tyr His Lys Leu Ser Asn Thr Glu Leu Glu Asn
690 695 700

Thr Glu Ser Ile Met Val Met Pro Tyr Pro Lys Asp Leu Ala Gln Asp
705 710 715 720

Glu Lys Leu Glu His Glu Phe Glu Val Ile Lys Asp Cys Ile Val Ser
725 730 735

Leu Arg Arg Leu Lys Ile Met Leu Glu Thr Pro Pro Ile Val Leu Lys
740 745 750

Glu Ala Ser Val Gly Leu Arg Glu Ala Ile Glu Asn Thr Glu Arg Leu
755 760 765

Gln Thr Tyr Ala Gln Lys Leu Ala Arg Leu Glu Lys Val Ser Val Ile
770 775 780

Ser Ser Lys Pro Leu Lys Ser Val Ser Asp Val Gly Glu Phe Cys Gln
785 790 795 800

Thr Tyr Ala Asn Leu Glu Asn Leu Asp Leu Ser Pro Leu Val Ala Arg
805 810 815

Leu Lys Lys Gln Leu Glu Lys Leu Glu Lys Glu Lys Leu Lys Leu Asn
820 825 830

Leu His Asn Glu Asn Phe Val Lys Asn Ala Pro Lys Ser Val Leu Glu
835 840 845

Lys Ala Lys Glu Ser Leu Lys Thr Leu Leu Glu Lys Glu Ser Lys Ile
850 855 860

Lys Gln Glu Leu Asp Leu Leu Glu Gln Pro
865 870

<210> 278

<211> 202

<212> PRT

<213> Helicobacter pylori

<400> 278

Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr Ala Ser Leu Val
1 5 10 15

Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys Glu Asn Gly Pro
20 25 30

His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val Cys Lys Ser Gly
35 40 45

Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr His Thr Gln Asp
50 55 60

Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys Pro Lys Ala Val
65 70 75 80

Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu Pro Thr Asn His
85 90 95

Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn Val His Phe His
100 105 110

Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg Pro Leu Ser Ala
115 120 125

His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu Val Leu Ala Ile
130 135 140

Gly Phe Glu Glu Gly Lys Glu Asn Pro Asn Leu Asp Pro Ile Leu Glu
145 150 155 160

Gly Ile Gln Lys Lys Gln Asn Phe Lys Glu Val Ala Leu Asp Ala Phe
165 170 175

Leu Pro Lys Ser Ile Asn Tyr Tyr His Leu Thr Ala Leu Ser Pro Leu
180 185 190

Leu Leu Ala Gln Arg Gly Trp His Gly Leu
195 200

<210> 279

<211> 2890

<212> PRT

<213> Helicobacter pylori

<400> 279

Met Ser Lys Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr
1 5 10 15

Lys Thr Pro Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg
20 25 30

Asp Ser Tyr Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly
35 40 45

Ile Glu Lys Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn
50 55 60

Arg Ile Thr Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr
65 70 75 80

Thr Val Arg Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu
85 90 95

Lys Ile Lys Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly
100 105 110

Glu Lys Asn Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg
115 120 125

Glu Ile Pro Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val
130 135 140

Glu Arg Val Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe
145 150 155 160

Lys Glu Glu Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly
165 170 175

Gln Ile Ile Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser
180 185 190

Lys Asp Val Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val
195 200 205

Thr Ile Leu Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys
210 215 220

Met Phe Tyr Pro Leu Val Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu
225 230 235 240

Ile Pro Phe Ala Ser Leu Asp Ala Asn Gln Arg Met Glu Phe Asp Leu
245 250 255

Lys Asp Pro Gln Gly Lys Val Ile Leu Leu Ala Gly Lys Lys Leu Thr
260 265 270

Ser Arg Lys Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu
275 280 285

Tyr Pro Met Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met
290 295 300

Val Gly Lys Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn
305 310 315 320

Lys Leu Glu Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile
325 330 335

Asn Asp Leu Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser
340 345 350

Ala Asp Ser Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp
355 360 365

Asp Glu Asn Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro
370 375 380

Gly Asp Pro Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu
385 390 395 400

Phe Phe Asp Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys
405 410 415

Met Asn His Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu
420 425 430

Thr His Glu Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys
435 440 445

Asn Asn Gln Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg
450 455 460

Ile Arg Ala Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu
465 470 475 480

Val Lys Met Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly
485 490 495

Ala Phe Asp Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile
500 505 510

Thr Ser Thr Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe
515 520 525

Met Asp Gln Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu
530 535 540

Ser Ala Leu Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu
545 550 555 560

Ala Arg Asp Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu
565 570 575

Thr Pro Glu Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe
580 585 590

Thr Arg Val Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val
595 600 605

Val Asp Gly Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln
610 615 620

Glu Asp Ser His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu
625 630 635 640

Gly Asn Ile Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile
645 650 655

Val Leu Asn Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser
660 665 670

Met Leu Val Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp
675 680 685

Asp Ala Asn Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val
690 695 700

Pro Leu Leu Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys
705 710 715 720

Ile Ile Ala Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly
725 730 735

Val Val Glu Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser
740 745 750

Lys Glu Glu Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg
755 760 765

Thr Asn Gln Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly
770 775 780

Asp Lys Val Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp
785 790 795 800

Arg Gly Glu Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro
805 810 815

Trp Asn Gly Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile
820 825 830

Thr Lys Asp Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val
835 840 845

Asp Ala Arg Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile
850 855 860

Pro Asp Val Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile
865 870 875 880

Val Lys Val Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys
885 890 895

Thr Ser Pro Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu
900 905 910

Arg Ala Ile Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu
915 920 925

Tyr Cys Pro Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe
930 935 940

Thr Lys Lys Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu
945 950 955 960

Glu Glu Lys Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met
965 970 975

Leu Asn Arg Glu Glu Leu Leu Arg Val Ser Ser Leu Leu Ser Gln Ala
980 985 990

Ile Leu Glu Glu Pro Phe Ser His Asn Gly Lys Asp Tyr Lys Glu Gly
995 1000 1005

Asp Gln Ile Pro Lys Glu Glu Ile Ala Ser Ile Asn Arg Phe Thr
1010 1015 1020

Leu Ala Ser Leu Val Lys Lys Tyr Ser Lys Glu Val Gln Asn His
1025 1030 1035

Tyr Glu Ile Thr Lys Asn Asn Phe Leu Glu Gln Lys Lys Val Leu
1040 1045 1050

Gly Glu Glu His Glu Glu Lys Leu Ser Ile Leu Glu Lys Asp Asp
1055 1060 1065

Ile Leu Pro Asn Gly Val Ile Lys Lys Val Lys Leu Tyr Ile Ala
1070 1075 1080

Thr Lys Arg Lys Leu Lys Val Gly Asp Lys Met Ala Gly Arg His
1085 1090 1095

Gly Asn Lys Gly Ile Val Ser Asn Ile Val Pro Val Ala Asp Met
1100 1105 1110

Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp Ile Val Leu Asn Pro
1115 1120 1125

Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln Ile Leu Glu Met
1130 1135 1140

His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln Ile Ala Arg
1145 1150 1155

Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu Arg Ala
1160 1165 1170

Lys Met Leu Glu Ile Ala Asn Ala Ile Asn Glu Lys Asp Pro Leu
1175 1180 1185

Thr Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu
1190 1195 1200

Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val
1205 1210 1215

Phe Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu
1220 1225 1230

Ala Lys Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg
1235 1240 1245

Thr Gly Glu Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met Tyr
1250 1255 1260

Met Ile Lys Leu His His Leu Val Asp Glu Lys Val His Ala Arg
1265 1270 1275

Ser Thr Gly Pro Tyr Ser Leu Val Thr His Gln Pro Val Gly Gly
1280 1285 1290

Lys Ala Leu Phe Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp
1295 1300 1305

Ala Leu Glu Ala Tyr Gly Ala Ala His Thr Leu Lys Glu Met Leu
1310 1315 1320

Thr Ile Lys Ser Asp Asp Ile Arg Gly Arg Glu Asn Ala Tyr Arg
1325 1330 1335

Ala Ile Ala Lys Gly Glu Gln Val Gly Glu Ser Glu Ile Pro Glu
1340 1345 1350

Thr Phe Tyr Val Leu Thr Lys Glu Leu Gln Ser Leu Ala Leu Asp
1355 1360 1365

Ile Asn Ile Phe Gly Asp Asp Val Asp Glu Asp Gly Ala Pro Lys
1370 1375 1380

Pro Ile Val Ile Lys Glu Asp Asp Arg Pro Lys Asp Phe Ser Ser
1385 1390 1395

Phe Gln Leu Thr Leu Ala Ser Pro Glu Lys Ile His Ser Trp Ser
1400 1405 1410

Tyr Gly Glu Val Lys Lys Pro Glu Thr Ile Asn Tyr Arg Thr Leu
1415 1420 1425

Lys Pro Glu Arg Asp Gly Leu Phe Cys Met Lys Ile Phe Gly Pro
1430 1435 1440

Thr Lys Asp Tyr Glu Cys Leu Cys Gly Lys Tyr Lys Lys Pro Arg
1445 1450 1455

Phe Lys Asp Ile Gly Thr Cys Glu Lys Cys Gly Val Ala Ile Thr
1460 1465 1470

His Ser Lys Val Arg Arg Phe Arg Met Gly His Ile Glu Leu Ala
1475 1480 1485

Thr Pro Val Ala His Ile Trp Tyr Val Asn Ser Leu Pro Ser Arg
1490 1495 1500

Ile Gly Thr Leu Leu Gly Val Lys Met Lys Asp Leu Glu Arg Val
1505 1510 1515

Leu Tyr Tyr Glu Ala Tyr Ile Val Lys Glu Pro Gly Glu Ala Ala
1520 1525 1530

Tyr Asp Asn Glu Gly Thr Lys Leu Val Met Lys Tyr Asp Ile Leu
1535 1540 1545

Asn Glu Glu Gln Tyr Gln Asn Ile Ser Arg Arg Tyr Glu Asp Arg
1550 1555 1560

Gly Phe Val Ala Gln Met Gly Gly Glu Ala Ile Lys Asp Leu Leu
1565 1570 1575

Glu Glu Ile Asp Leu Ile Thr Leu Leu Gln Ser Leu Lys Glu Glu
1580 1585 1590

Val Lys Asp Thr Asn Ser Asp Ala Lys Lys Lys Lys Leu Ile Lys
1595 1600 1605

Arg Leu Lys Val Val Glu Ser Phe Leu Asn Ser Gly Asn Arg Pro
1610 1615 1620

Glu Trp Met Met Leu Thr Val Leu Pro Val Leu Pro Pro Asp Leu
1625 1630 1635

Arg Pro Leu Val Ala Leu Asp Gly Gly Lys Phe Ala Val Ser Asp
1640 1645 1650

Val Asn Glu Leu Tyr Arg Arg Val Ile Asn Arg Asn Gln Arg Leu
1655 1660 1665

Lys Arg Leu Met Glu Leu Gly Ala Pro Glu Ile Ile Val Arg Asn
1670 1675 1680

Glu Lys Arg Met Leu Gln Glu Ala Val Asp Val Leu Phe Asp Asn
1685 1690 1695

Gly Arg Ser Thr Asn Ala Val Lys Gly Ala Asn Lys Arg Pro Leu
1700 1705 1710

Lys Ser Leu Ser Glu Ile Ile Lys Gly Lys Gln Gly Arg Phe Arg
1715 1720 1725

Gln Asn Leu Leu Gly Lys Arg Val Asp Phe Ser Gly Arg Ser Val
1730 1735 1740

Ile Val Val Gly Pro Asn Leu Lys Met Asp Glu Cys Gly Leu Pro
1745 1750 1755

Lys Asn Met Ala Leu Glu Leu Phe Lys Pro His Leu Leu Ser Lys
1760 1765 1770

Leu Glu Glu Arg Gly Tyr Ala Thr Thr Leu Lys Gln Ala Lys Arg
1775 1780 1785

Met Ile Glu Gln Lys Ser Asn Glu Val Trp Glu Cys Leu Gln Glu
1790 1795 1800

Ile Thr Glu Gly Tyr Pro Val Leu Leu Asn Arg Ala Pro Thr Leu
1805 1810 1815

His Lys Gln Ser Ile Gln Ala Phe His Pro Lys Leu Ile Asp Gly
1820 1825 1830

Lys Ala Ile Gln Leu His Pro Leu Val Cys Ser Ala Phe Asn Ala
1835 1840 1845

Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu Ser Gln
1850 1855 1860

Glu Ala Ile Ala Glu Cys Lys Val Leu Met Leu Ser Ser Met Asn
1865 1870 1875

Ile Leu Leu Pro Ala Ser Gly Lys Ala Val Ala Ile Pro Ser Gln
1880 1885 1890

Asp Met Val Leu Gly Leu Tyr Tyr Leu Ser Leu Glu Lys Ser Gly
1895 1900 1905

Val Lys Gly Glu His Lys Leu Phe Ser Ser Val Asn Glu Ile Ile
1910 1915 1920

Thr Ala Ile Asp Thr Lys Glu Leu Asp Ile His Ala Lys Ile Arg
1925 1930 1935

Val Leu Asp Gln Gly Asn Ile Ile Ala Thr Ser Ala Gly Arg Met
1940 1945 1950

Ile Ile Lys Ser Ile Leu Pro Asp Phe Ile Pro Thr Asp Leu Trp
1955 1960 1965

Asn Arg Pro Met Lys Lys Lys Asp Ile Gly Val Leu Val Asp Tyr
1970 1975 1980

Val His Lys Val Gly Gly Ile Gly Ile Thr Ala Thr Phe Leu Asp
1985 1990 1995

Asn Leu Lys Thr Leu Gly Phe Arg Tyr Ala Thr Lys Ala Gly Ile
2000 2005 2010

Ser Ile Ser Met Glu Asp Ile Ile Thr Pro Lys Asp Lys Gln Lys
2015 2020 2025

Met Val Glu Lys Ala Lys Val Glu Val Lys Lys Ile Gln Gln Gln
2030 2035 2040

Tyr Asp Gln Gly Leu Leu Thr Asp Gln Glu Arg Tyr Asn Lys Ile
2045 2050 2055

Ile Asp Thr Trp Thr Glu Val Asn Asp Lys Met Ser Lys Glu Met
2060 2065 2070

Met Thr Ala Ile Ala Gln Asp Lys Glu Gly Phe Asn Ser Ile Tyr
2075 2080 2085

Met Met Ala Asp Ser Gly Ala Arg Gly Ser Ala Ala Gln Ile Arg
2090 2095 2100

Gln Leu Ser Ala Met Arg Gly Leu Met Thr Lys Pro Asp Gly Ser
2105 2110 2115

Ile Ile Glu Thr Pro Ile Ile Ser Asn Phe Lys Glu Gly Leu Asn
2120 2125 2130

Val Leu Glu Tyr Phe Asn Ser Thr His Gly Ala Arg Lys Gly Leu
2135 2140 2145

Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala Gly Tyr Leu Thr Arg
2150 2155 2160

Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val Val Ser Asp Asp
2165 2170 2175

Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile Ala Val Gly
2180 2185 2190

Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly Arg Val
2195 2200 2205

Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu Leu
2210 2215 2220

Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val
2225 2230 2235

Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys
2240 2245 2250

Lys Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu
2255 2260 2265

Gly Glu Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val
2270 2275 2280

Ala Ala Gln Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg
2285 2290 2295

Thr Phe His Val Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg
2300 2305 2310

Glu Ile Val Ala Ser Lys Glu Gly Phe Val Arg Phe Tyr Asn Leu
2315 2320 2325

Arg Thr Tyr Thr Asn Lys Glu Gly Lys Asn Ile Ile Ala Asn Arg
2330 2335 2340

Arg Asn Ala Ser Ile Leu Val Val Glu Pro Lys Ile Lys Ala Pro
2345 2350 2355

Phe Asp Gly Glu Leu Arg Ile Glu Thr Val Tyr Glu Glu Val Val
2360 2365 2370

Val Ser Val Lys Asn Gly Asp Gln Glu Ala Lys Phe Val Leu Arg
2375 2380 2385

Arg Ser Asp Ile Val Lys Pro Ser Glu Leu Ala Gly Val Gly Gly
2390 2395 2400

Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala Ser Gly His Lys
2405 2410 2415

Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln Glu Gly Trp
2420 2425 2430

Asn Val Pro Asn Arg Ile Pro Tyr Ala Ser Glu Leu Leu Val Lys
2435 2440 2445

Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys Gly
2450 2455 2460

Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr
2465 2470 2475

His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe
2480 2485 2490

Ala Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr
2495 2500 2505

Ile Ala Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val
2510 2515 2520

Ser Thr Asn Ser Val Ile Ser Lys Pro Thr Thr Asn Thr Phe Lys
2525 2530 2535

Thr Ile Ala Thr Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp
2540 2545 2550

Phe Lys Gly Lys Val Gly Phe Val Asp Val Ile Ala Gly Val Thr
2555 2560 2565

Val Ala Glu Lys Glu Asp Glu Asn Thr Gly Ile Thr Ser Leu Val
2570 2575 2580

Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe Leu
2585 2590 2595

Glu Gly Ala Asn Gly Glu Glu Met Arg Tyr Phe Leu Glu Pro Lys
2600 2605 2610

Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu
2615 2620 2625

Val Leu Ala Lys Ile Pro Lys Ala Thr Val Lys Ser Arg Asp Ile
2630 2635 2640

Thr Gly Gly Leu Pro Arg Val Ser Glu Leu Phe Glu Ala Arg Lys
2645 2650 2655

Pro Lys Pro Lys Asp Val Ala Ile Leu Ser Glu Val Asp Gly Ile
2660 2665 2670

Val Ser Phe Gly Lys Pro Ile Arg Asn Lys Glu His Ile Ile Val
2675 2680 2685

Thr Ser Lys Asp Gly Arg Ser Met Asp Tyr Phe Val Asp Lys Gly
2690 2695 2700

Lys Gln Ile Leu Val His Ala Asp Glu Phe Val His Ala Gly Glu
2705 2710 2715

Ala Met Thr Asp Gly Val Ile Ser Ser His Asp Ile Leu Arg Ile
2720 2725 2730

Ser Gly Glu Lys Glu Leu Tyr Lys Tyr Ile Val Ser Glu Val Gln
2735 2740 2745

Gln Val Tyr Arg Arg Gln Gly Val Ser Ile Ala Asp Lys His Ile
2750 2755 2760

Glu Ile Ile Val Ser Gln Met Leu Arg Gln Val Arg Ile Leu Asp
2765 2770 2775

Ser Gly Asp Ser Lys Phe Ile Glu Gly Asp Leu Val Ser Lys Lys
2780 2785 2790

Leu Phe Lys Glu Glu Asn Ala Arg Val Ile Ala Leu Lys Gly Glu
2795 2800 2805

Pro Ala Ile Ala Glu Pro Val Leu Leu Gly Ile Thr Arg Ala Ala
2810 2815 2820

Ile Gly Ser Asp Ser Ile Ile Ser Ala Ala Ser Phe Gln Glu Thr
2825 2830 2835

Thr Lys Val Leu Thr Glu Ala Ser Ile Ala Met Lys Lys Asp Phe
2840 2845 2850

Leu Glu Asp Leu Lys Glu Asn Val Val Leu Gly Arg Met Ile Pro
2855 2860 2865

Val Gly Thr Gly Met Tyr Lys Asn Lys Lys Ile Val Leu Arg Ala
2870 2875 2880

Leu Glu Asp Asn Ser Lys Phe
2885 2890

<210> 280

<211> 399

<212> PRT

<213> Helicobacter pylori

<400> 280

Met Ala Lys Glu Lys Phe Asn Arg Thr Lys Pro His Val Asn Ile Gly
1 5 10 15

Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Ser Ala Ala Ile
20 25 30

Ser Ala Val Leu Ser Leu Lys Gly Leu Ala Glu Met Lys Asp Tyr Asp
35 40 45

Asn Ile Asp Asn Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Ala
50 55 60

Thr Ser His Ile Glu Tyr Glu Thr Glu Asn Arg His Tyr Ala His Val
65 70 75 80

Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
85 90 95

Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Ala Asp Gly Pro
100 105 110

Met Pro Gln Thr Arg Glu His Ile Leu Leu Ser Arg Gln Val Gly Val
115 120 125

Pro His Ile Val Val Phe Leu Asn Lys Gln Asp Met Val Asp Asp Gln
130 135 140

Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Ala
145 150 155 160

Tyr Glu Phe Pro Gly Asp Asp Thr Pro Ile Val Ala Gly Ser Ala Leu
165 170 175

Arg Ala Leu Glu Glu Ala Lys Ala Gly Asn Val Gly Glu Trp Gly Glu
180 185 190

Lys Val Leu Lys Leu Met Ala Glu Val Asp Ala Tyr Ile Pro Thr Pro
195 200 205

Glu Arg Asp Thr Glu Lys Thr Phe Leu Met Pro Val Glu Asp Val Phe
210 215 220

Ser Ile Ala Gly Arg Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly
225 230 235 240

Val Val Lys Val Gly Asp Glu Val Glu Ile Val Gly Ile Arg Pro Thr
245 250 255

Gln Lys Thr Thr Val Thr Gly Val Glu Met Phe Arg Lys Glu Leu Glu
260 265 270

Lys Gly Glu Ala Gly Asp Asn Val Gly Val Leu Leu Arg Gly Thr Lys
275 280 285

Lys Glu Glu Val Glu Arg Gly Met Val Leu Cys Lys Pro Gly Ser Ile
290 295 300

Thr Pro His Lys Lys Phe Glu Gly Glu Ile Tyr Val Leu Ser Lys Glu
305 310 315 320

Glu Gly Gly Arg His Thr Pro Phe Phe Thr Asn Tyr Arg Pro Gln Phe
325 330 335

Tyr Val Arg Thr Thr Asp Val Thr Gly Ser Ile Thr Leu Pro Glu Gly
340 345 350

Val Glu Met Val Met Pro Gly Asp Asn Val Lys Ile Thr Val Glu Leu
355 360 365

Ile Ser Pro Val Ala Leu Glu Leu Gly Thr Lys Phe Ala Ile Arg Glu
370 375 380

Gly Gly Arg Thr Val Gly Ala Gly Val Val Ser Asn Ile Ile Glu
385 390 395

<210> 281

<211> 405

<212> PRT

<213> Helicobacter pylori

<400> 281

Val Leu Ile Val Gln Lys Tyr Gly Gly Thr Ser Met Gly Ser Ile Glu
1 5 10 15

Arg Ile His Asn Val Ala Gln Arg Val Leu Glu Ser Val Thr Leu Gly
20 25 30

His Gln Val Val Val Val Val Ser Ala Met Ser Gly Glu Thr Asp Arg
35 40 45

Leu Leu Glu Phe Gly Lys Asn Phe Ser His Asn Pro Asn Lys Arg Glu
50 55 60

Met Asp Arg Ile Val Ser Val Gly Glu Leu Val Ser Ser Ala Ala Leu
65 70 75 80

Ser Met Ala Leu Glu Arg Tyr Gly His Arg Ala Ile Ser Leu Ser Gly
85 90 95

Lys Glu Ala Gly Ile Leu Thr Ser Ser His Phe Gln Asn Ala Val Ile
100 105 110

Gln Ser Ile Asp Thr Lys Arg Ile Thr Glu Leu Leu Glu Lys Asn Tyr
115 120 125

Ile Val Val Ile Ala Gly Phe Gln Gly Ala Asp Ile Gln Gly Glu Thr
130 135 140

Thr Thr Leu Gly Arg Gly Gly Ser Asp Leu Ser Ala Val Ala Leu Ala
145 150 155 160

Gly Ala Leu Lys Ala His Leu Cys Glu Ile Tyr Thr Asp Val Asp Gly
165 170 175

Val Tyr Thr Thr Asp Pro Arg Ile Glu Glu Lys Ala Gln Lys Ile Ala
180 185 190

Gln Ile Ser Tyr Asp Glu Met Leu Glu Leu Ala Ser Met Gly Ala Lys
195 200 205

Val Leu Leu Asn Arg Ser Val Glu Leu Ala Lys Lys Leu Ser Val Lys
210 215 220

Leu Val Thr Arg Asn Ser Phe Asn His Ser Glu Gly Thr Leu Ile Val
225 230 235 240

Ala Glu Lys Asp Phe Lys Gly Glu Arg Met Glu Thr Pro Ile Val Ser
245 250 255

Gly Ile Ala Leu Asp Lys Asn Gln Ala Arg Val Ser Met Glu Gly Val
260 265 270

Glu Asp Arg Pro Gly Ile Ala Ala Glu Ile Phe Gly Ala Leu Ala Glu
275 280 285

Tyr Arg Ile Asn Val Asp Met Ile Val Gln Thr Ile Gly Arg Asp Gly
290 295 300

Lys Thr Asp Leu Asp Phe Thr Ile Val Lys Thr Gln Ile Glu Glu Thr
305 310 315 320

Lys Gln Ala Leu Lys Pro Phe Leu Ala Gln Met Asp Ser Ile Asp Tyr
325 330 335

Asp Glu Asn Ile Ala Lys Val Ser Ile Val Gly Val Gly Met Lys Ser
340 345 350

His Ser Gly Val Ala Ser Ile Ala Phe Lys Ala Leu Ala Lys Asp Asn
355 360 365

Ile Asn Ile Met Met Ile Ser Thr Ser Glu Ile Lys Ile Ser Val Leu
370 375 380

Ile Asp Ile Lys Tyr Ala Glu Leu Ala Val Arg Thr Leu His Ala Val
385 390 395 400

Tyr Gln Leu Asp Gln
405

<210> 282

<211> 733

<212> PRT

<213> Helicobacter pylori

<400> 282

Met Lys Lys His Ile Leu Ser Leu Ala Leu Gly Ser Leu Leu Val Ser
1 5 10 15

Thr Leu Ser Ala Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln
20 25 30

Ile Gly Glu Ala Ala Gln Met Val Thr Asn Thr Lys Gly Ile Gln Gln
35 40 45

Leu Ser Asp Asn Tyr Glu Asn Leu Asn Asn Leu Leu Thr Arg Tyr Ser
50 55 60

Thr Leu Asn Thr Leu Ile Lys Leu Ser Ala Asp Pro Ser Ala Ile Asn
65 70 75 80

Ala Val Arg Glu Asn Leu Gly Ala Ser Ala Lys Asn Leu Ile Gly Asp
85 90 95

Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Leu Leu Ala Ile Asn Ala
100 105 110

Ala Val Gly Phe Trp Asn Val Val Gly Tyr Val Thr Gln Cys Gly Gly
115 120 125

Asn Ala Asn Gly Gln Glu Ser Thr Ser Ser Thr Thr Ile Phe Asn Asn
130 135 140

Glu Pro Gly Tyr Arg Ser Thr Ser Ile Thr Cys Ser Leu Asn Gly His
145 150 155 160

Lys Pro Gly Tyr Tyr Gly Pro Met Ser Ile Glu Asn Phe Lys Lys Leu
165 170 175

Asn Glu Ala Tyr Gln Ile Leu Gln Thr Ala Leu Lys Asn Gly Leu Pro
180 185 190

Ala Leu Lys Glu Asn Asn Gly Lys Val Ser Val Thr Tyr Thr Tyr Thr
195 200 205

Cys Ser Gly Gln Gly Asn Asn Asn Cys Ser Pro Ser Val Asn Gly Thr
210 215 220

Lys Thr Thr Thr Gln Thr Ile Asp Gly Lys Ser Val Thr Thr Thr Ile
225 230 235 240

Ser Ser Lys Val Val Gly Ser Ile Ala Ser Gly Asn Thr Ser His Val
245 250 255

Ile Thr Asn Lys Leu Asp Gly Val Pro Asp Ser Ala Gln Ala Leu Leu
260 265 270

Ala Gln Ala Ser Thr Leu Ile Asn Thr Ile Asn Glu Ala Cys Pro Tyr
275 280 285

Phe His Ala Thr Asn Ser Ser Glu Ala Asn Ala Pro Lys Phe Ser Thr
290 295 300

Thr Thr Gly Lys Ile Cys Gly Ala Phe Ser Glu Glu Ile Ser Ala Ile
305 310 315 320

Gln Lys Met Ile Thr Asp Ala Gln Glu Leu Val Asn Gln Thr Ser Val
325 330 335

Ile Asn Ser Asn Glu Gln Ser Thr Pro Val Gly Asn Asn Asn Gly Lys
340 345 350

Pro Phe Asn Pro Phe Thr Asp Ala Ser Phe Ala Gln Gly Met Leu Ala
355 360 365

Asn Ala Ser Ala Gln Ala Lys Met Leu Asn Leu Ala His Gln Val Gly
370 375 380

Gln Ala Ile Asn Pro Glu Asn Leu Ser Glu Asn Phe Lys Asn Phe Val
385 390 395 400

Thr Gly Phe Leu Ala Thr Cys Asn Asn Lys Ser Thr Ala Gly Thr Gly
405 410 415

Gly Thr Gln Gly Ser Ala Pro Gly Thr Val Thr Thr Gln Thr Phe Ala
420 425 430

Ser Gly Cys Ala Tyr Val Glu Gln Thr Leu Thr Asn Leu Gly Asn Ser
435 440 445

Ile Ala His Phe Gly Thr Gln Glu Gln Gln Ile Gln Gln Ala Glu Asn
450 455 460

Ile Ala Asp Thr Leu Val Asn Phe Lys Ser Arg Tyr Ser Glu Leu Gly
465 470 475 480

Asn Thr Tyr Asn Ser Ile Thr Thr Ala Leu Ser Lys Val Pro Asn Ala
485 490 495

Gln Ser Leu Gln Asn Val Val Ser Lys Lys Asn Asn Pro Tyr Ser Pro
500 505 510

Gln Gly Ile Glu Thr Asn Tyr Tyr Leu Asn Gln Asn Ser Tyr Asn Gln
515 520 525

Ile Gln Thr Ile Asn Gln Glu Leu Gly Arg Asn Pro Phe Arg Lys Val
530 535 540

Gly Ile Val Asn Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile Gly
545 550 555 560

Ile Gln Val Gly Tyr Lys Gln Phe Phe Gly Gln Lys Arg Lys Trp Gly
565 570 575

Ala Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Phe Ile Lys Ser
580 585 590

Ser Phe Phe Asn Ser Ala Ser Asp Val Trp Thr Tyr Gly Phe Gly Ala
595 600 605

Asp Ala Leu Tyr Asn Phe Ile Asn Asp Lys Ala Thr Asn Phe Leu Gly
610 615 620

Lys Asn Asn Lys Leu Ser Leu Gly Leu Phe Gly Gly Ile Ala Leu Ala
625 630 635 640

Gly Thr Ser Trp Leu Asn Ser Glu Tyr Val Asn Leu Ala Thr Val Asn
645 650 655

Asn Val Tyr Asn Ala Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe
660 665 670

Asn Met Gly Val Arg Met Asn Leu Ala Arg Ser Lys Lys Lys Gly Ser
675 680 685

Asp His Ala Ala Gln His Gly Ile Glu Leu Gly Leu Lys Ile Pro Thr
690 695 700

Ile Asn Thr Asn Tyr Tyr Ser Phe Met Gly Ala Glu Leu Lys Tyr Arg
705 710 715 720

Arg Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr
725 730

<210> 283

<211> 240

<212> PRT

<213> Helicobacter pylori

<400> 283

Leu Asp Ser Phe His Ser Phe Asn Gln His Ala Phe Asn Arg His Ala
1 5 10 15

Lys Thr Tyr His Leu Phe Ala His Ile Gln Gln Gln Ile Ala Ile Cys
20 25 30

Leu Val Gln Phe Leu Lys Gln Lys His Tyr Ala Lys Val Leu Asp Leu
35 40 45

Gly Ser Gly Ser Gly Ala Val Phe Asn Ala Leu Glu Arg Gln Asn Ile
50 55 60

Leu Ile Glu Glu Phe Ile Ala Leu Asp Asn Ser Ile Asn Met Leu Lys
65 70 75 80

Leu His Pro Thr His Ser Ile Asn Ile Gln Lys Ile Ser Leu Glu His
85 90 95

Ala Asp Phe Glu Glu His Val Phe Cys Thr Tyr Asp Leu Val Val Ser
100 105 110

Ser Ser Ser Leu Gln Trp Ala Arg Asp Leu Lys Ser Val Leu Glu Lys
115 120 125

Ile Ala Leu Ser Ser Lys Glu Val Ala Leu Ala Ile His Thr Asp Phe
130 135 140

Ser Leu His Glu Val His Glu Phe Leu Gly Thr Pro Ser Pro Leu Arg
145 150 155 160

Asp Leu Lys Thr Leu Lys Ser Leu Ile Lys Asn Ala Phe Lys His Phe
165 170 175

Gln Ile Glu Leu Glu Asn Lys Arg Phe Ala Leu Tyr Phe Asn Arg Lys
180 185 190

Gln Asp Cys Leu Asn Tyr Leu Lys Lys Cys Gly Leu Leu Gly Gly Ser
195 200 205

Thr Leu Ser Phe Lys Gln Lys Lys His Phe Phe Gln Asn Met Ala Phe
210 215 220

Glu Lys Leu Ser Tyr Glu Val Leu Leu Phe Ser Gly Ile Lys Arg Ser
225 230 235 240

<210> 284

<211> 328

<212> PRT

<213> Helicobacter pylori

<400> 284

Leu Ser Gly Phe Asn Pro Leu Asn Ser Pro Leu Val Ala Ser Ser Ser
1 5 10 15

Leu Ser Leu Lys Glu Ala Tyr Tyr Leu Glu Lys Leu Ser Leu Lys Lys
20 25 30

Gly Phe Lys Ile His Tyr Lys Met Thr Lys Asp Ser Leu Asn Leu Leu
35 40 45

Glu Lys Ser Asp Leu Cys Val Leu Phe Gly Gly Phe Ser Asn Ala Cys
50 55 60

Leu Asn Glu Asn Glu Arg Trp Ile Leu Glu Ser Ile Ser His Ser Lys
65 70 75 80

Arg Pro Tyr Ala Leu Leu Arg Pro Leu Gln Asp Thr Arg Asp Leu Gln
85 90 95

Glu Asn Cys Leu Phe Ala Ser Tyr Glu Ile His Thr Glu Ala Ala Ile
100 105 110

Leu Ala Leu Ile Leu Arg Gly Ile Leu Glu Gln Thr Ser Gln Leu Lys
115 120 125

Gly His Val Leu Glu Lys Ile Asp Val Gly Tyr Leu Ser Ser Glu Ala
130 135 140

Asn Met Ser Glu Glu Glu Leu Gln Glu Leu Ile Ala Leu Ile Val Lys
145 150 155 160

Ala Lys Lys Arg Ala Leu Val Leu Asn Arg Glu Ile Thr Lys His Ala
165 170 175

Asn Asn Ala Phe Leu Tyr Thr Leu Leu Ser Glu Leu Gln Asn Tyr Leu
180 185 190

Glu Ile Leu His Ile Pro Cys Tyr Asp Ser Ser Ala Thr Thr Ala Phe
195 200 205

Tyr Asp Phe Lys Asp Gln Glu Trp Leu Leu Glu Thr Ala Phe Lys Glu
210 215 220

Gly Ile Leu Pro Phe Lys Ser Gln Leu Gln Ser Lys Asp Leu Glu Leu
225 230 235 240

Leu Glu Arg Ile Ser Glu Ala Asn Gly Ser Phe Val Tyr Val Ser Tyr
245 250 255

Lys Ser Leu Glu Thr Pro Lys Leu Ser Phe Ser Lys Gln Phe Lys Ile
260 265 270

Ala Asn Lys Ile Glu His Ser Lys Ala Gly Phe Gln Ile Ser Asn Gln
275 280 285

Thr Leu Glu Cys Glu Leu Glu Glu Asn Pro His Leu Lys Gly Leu Ile
290 295 300

Ala Ile Leu Glu Gly Ala Phe Phe Asp Ala Tyr Pro Tyr Ile Pro Ile
305 310 315 320

Leu Ser His Ser Gln Gly Ile Ser
325

<210> 285

<211> 500

<212> PRT

<213> Helicobacter pylori

<400> 285

Met Ile Ser Leu Ile Glu Lys Ala Pro Tyr Ile Pro Tyr Pro Leu Ala
1 5 10 15

Leu Tyr Glu Lys Leu Glu Gln Pro His Thr Leu Leu Phe Glu Ser Ala
20 25 30

Glu Ile Glu Ser Lys Ala His Thr Lys Ser Leu Leu Met Ala Lys Ala
35 40 45

Cys Leu Lys Leu Ile Cys Asn His Asn Ile Val Thr Ile Thr Ser Leu
50 55 60

Thr Pro Asn Gly Gly Ala Phe Leu Gln Lys Leu Ser Ala Phe Phe Lys
65 70 75 80

Thr Pro Ile Gln Asp Asn Ala Leu Ile Leu Thr Tyr Thr Lys Asn Lys
85 90 95

Lys Thr Gln Asp Glu Phe Leu Lys Leu Phe Glu Pro Ser Pro Phe Asp
100 105 110

Ala Leu Arg Gly Leu Phe Lys Ser Val Lys Thr Lys Pro Lys His Pro
115 120 125

Phe Thr Leu Leu Ser Ala Gly Val Phe Ser Phe Glu Met Leu Asn Phe
130 135 140

Phe Glu Asp Leu Pro His Leu Lys Ala Lys Asp Asn Thr Val His Asp
145 150 155 160

Phe Ile Phe Tyr Leu Ala Gln Asn Leu Ile Ile Ile Asp His Lys Glu
165 170 175

Lys Ser Val Glu Ile Leu Gly Ala Cys Phe Asp Glu Arg Phe Lys Thr
180 185 190

Glu Ile Ala Gln Glu Leu Gln Asp Leu Lys Glu Leu Ala Lys Ser Ile
195 200 205

Lys Ser Asp Phe Val Pro Lys Lys Ser Lys Gln Ser Arg Glu Val Ser
210 215 220

Ala Asn Cys Ser Asp Ser Glu Phe Glu Lys Arg Val Leu Ser Leu Gln
225 230 235 240

Glu Glu Ile Lys Lys Gly Glu Ile Phe Gln Ala Val Leu Ser Arg Ser
245 250 255

Phe Tyr Met Glu Cys Leu Glu Gly Leu Ser Ala Tyr Tyr His Leu Lys
260 265 270

Leu Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Lys Asp Ser Asp Phe
275 280 285

Ile Leu Phe Gly Ala Ser Pro Glu Ser Ala Leu Lys Tyr Asn Ala Leu
290 295 300

Thr Asn Thr Ala Glu Ile Tyr Pro Ile Ala Gly Thr Arg Leu Arg Gly
305 310 315 320

Lys Asp Lys Gln Gly Asn Ile Asp Tyr Asp Leu Asp Ser Lys Met Glu
325 330 335

Phe Asp Leu Gln His Asp Tyr Lys Glu Arg Ala Glu His Ile Met Leu
340 345 350

Val Asp Leu Ala Arg Asn Asp Met Ala Arg Val Ser Lys Lys Arg Tyr
355 360 365

Cys Asp Lys Leu Leu Lys Val Asp Lys Tyr Ser Asn Val Met His Leu
370 375 380

Val Ser Arg Val Val Gly Glu Leu Lys Lys Gly Cys Asp Ser Leu His
385 390 395 400

Ala Tyr Arg Ser Phe Met Asn Ala Gly Thr Leu Ser Gly Ala Pro Lys
405 410 415

Ile Ser Ala Ile Arg Leu Ile Tyr Gln Leu Glu Asn Gln Arg Arg Gly
420 425 430

Ser Tyr Gly Gly Ser Val Gly Tyr Leu Asn Ser Glu Gly Ser Met Asp
435 440 445

Ser Cys Ile Thr Ile Arg Ser Cys Phe Val Lys Asn Asn Arg Ala Val
450 455 460

Ile Gln Ala Gly Ala Gly Ile Val Leu Asp Ser Val Pro Gln Asn Glu
465 470 475 480

Ala Asn Glu Thr Arg Ala Lys Ala Gln Ala Leu Ile Asp Ala Ile Arg
485 490 495

Lys Thr Ser Leu
500

<210> 286

<211> 1035

<212> PRT

<213> Helicobacter pylori

<400> 286

Met Ile Glu Lys Ile Ile Asp Leu Ser Val Lys Asn Lys Leu Leu Thr
1 5 10 15

Thr Leu Val Thr Leu Leu Ile Phe Leu Ala Ser Leu Trp Ala Ile Lys
20 25 30

Ser Val Arg Leu Asp Ala Leu Pro Asp Leu Ser Pro Ala Gln Val Val
35 40 45

Val Gln Ile Thr Tyr Pro Asn Gln Ser Pro Lys Ile Val Gln Glu Gln
50 55 60

Val Thr Tyr Pro Leu Val Ser Thr Phe Met Ser Ile Ala Asn Ile Asp
65 70 75 80

Thr Val Arg Gly Ile Ser Ser Tyr Glu Ser Gly Leu Ile Tyr Ile Ile
85 90 95

Phe Lys Asp Gly Val Asn Leu Tyr Trp Ala Arg Asp Arg Val Leu Glu
100 105 110

Gln Leu Asn Arg Val Ser Asn Leu Pro Lys Asp Ala Lys Val Glu Ile
115 120 125

Gly Ser Asp Ser Thr Ser Ile Gly Trp Ala Tyr Gln Tyr Ala Leu Ser
130 135 140

Ser Asp Ser Lys Asn Leu Ser Asp Leu Lys Val Leu Gln Asp Phe Tyr
145 150 155 160

Tyr Arg Tyr Ala Leu Leu Gly Val Asp Gly Val Ser Glu Val Ala Ser
165 170 175

Val Gly Gly Phe Val Lys Asp Tyr Glu Val Thr Leu Gln Asn Asp Ser
180 185 190

Leu Ile Arg Tyr Asn Leu Ser Leu Glu Gln Val Ala Asn Ala Ile Lys
195 200 205

Asn Ser Asn Asn Asp Thr Gly Gly Gly Val Ile Leu Glu Asn Gly Phe
210 215 220

Glu Lys Ile Ile Arg Ser His Gly Tyr Ile Gln Ser Leu Lys Asp Leu
225 230 235 240

Glu Glu Ile Val Val Lys Lys Glu Gly Ala Ile Pro Leu Lys Ile Lys
245 250 255

Asp Ile Ala Ser Val Arg Leu Thr Pro Lys Pro Arg Arg Gly Ala Ala
260 265 270

Asn Leu Asn Gly Asp Lys Glu Val Val Gly Gly Ile Val Met Val Arg
275 280 285

Tyr His Ala Asp Thr Tyr Lys Val Leu Lys Ala Ile Lys Glu Lys Ile
290 295 300

Ala Thr Leu Gln Ala Ser Asn Pro Asp Val Lys Ile Thr Ser Val Tyr
305 310 315 320

Asp Arg Ser Glu Leu Ile Glu Lys Gly Ile Asp Asn Leu Ile His Thr
325 330 335

Leu Ile Glu Glu Ser Val Ile Val Leu Val Ile Ile Ala Ile Phe Leu
340 345 350

Leu His Phe Arg Ser Ala Leu Val Val Ile Ile Thr Leu Pro Leu Ser
355 360 365

Val Cys Ile Ser Phe Leu Leu Met Arg Tyr Phe Asn Ile Glu Ala Ser
370 375 380

Ile Met Ser Leu Gly Gly Ile Ala Ile Ala Ile Gly Ala Met Val Asp
385 390 395 400

Ala Ala Ile Val Met Val Glu Asn Ala His Lys His Leu Gln His Ile
405 410 415

Asp Val Lys Asp Asn Ala Gln Arg Val Asn Gly Ile Ile Glu Gly Val
420 425 430

Lys His Val Gly Gly Ala Ile Phe Phe Ala Leu Met Ile Ile Val Val
435 440 445

Ser Phe Leu Pro Ile Phe Ala Leu Thr Gly Gln Glu Glu Lys Leu Phe
450 455 460

Ala Pro Leu Ala Tyr Thr Lys Thr Phe Ala Met Leu Val Gly Ala Leu
465 470 475 480

Leu Ser Ile Thr Met Val Pro Ile Leu Met Val Trp Leu Ile Lys Gly
485 490 495

Arg Ile Leu Glu Glu Ser Lys Asn Pro Ile Asn Ala Phe Phe Met Lys
500 505 510

Ile Tyr Gly Val Ser Leu Asn Val Val Leu Lys Phe Arg Tyr Ala Phe
515 520 525

Leu Ile Ala Ser Val Leu Gly Leu Gly Gly Leu Tyr Val Ala Tyr Lys
530 535 540

Lys Leu Asn Trp Glu Phe Ile Pro Gln Ile Asn Glu Gly Val Val Met
545 550 555 560

Tyr Met Pro Val Thr Ile Asn Gly Val Ser Ile Asp Thr Ala Leu Glu
565 570 575

Tyr Leu Lys Lys Ser Asn Ser Ala Ile Lys Arg Leu Asp Phe Val Lys
580 585 590

Gln Val Phe Gly Lys Val Gly Arg Ala Asn Thr Ser Thr Asp Ala Ala
595 600 605

Gly Leu Ser Met Ile Glu Thr Tyr Ile Glu Leu Lys Pro Gln Asn Glu
610 615 620

Trp Lys Glu Lys Leu Ser Tyr Lys Glu Val Arg Asp Lys Leu Glu Lys
625 630 635 640

Thr Leu Gln Leu Lys Gly Leu Thr Asn Ser Trp Thr Tyr Pro Ile Arg
645 650 655

Gly Arg Thr Asp Met Leu Leu Thr Gly Ile Arg Thr Pro Leu Gly Ile
660 665 670

Lys Leu Tyr Gly Asn Asp Thr Asp Lys Leu Gln Glu Leu Ala Ile Leu
675 680 685

Met Glu Gln Gln Leu Lys Thr Leu Lys Glu Ser Leu Ser Val Phe Ala
690 695 700

Glu Arg Ser Asn Asn Gly Tyr Tyr Ile Thr Leu Asp Leu Asn Asp Glu
705 710 715 720

Asn Leu Ala Arg Tyr Gly Ile Asn Lys Lys Ala Val Leu Asp Ala Ile
725 730 735

Lys Phe Ala Leu Gly Gly Ala Thr Leu Thr Thr Met Ile Lys Gly Val
740 745 750

Glu Asn Tyr Pro Ile Ser Leu Arg Leu Glu Asp Thr Glu Arg Asn Thr
755 760 765

Ile Glu Lys Leu Lys Asn Leu Tyr Ile Lys Thr Ala Tyr Asn Tyr Met
770 775 780

Pro Leu Arg Glu Leu Ala Arg Ile Tyr Tyr Asp Asn Ser Pro Ala Val
785 790 795 800

Leu Lys Ser Glu Lys Gly Leu Asn Val Asn Phe Ile Tyr Ile Val Pro
805 810 815

Gln Asn Gly Ile Ser Ser Asp Ala Tyr Arg Gln Leu Ala Gln Lys Ala
820 825 830

Leu Glu Lys Ile Gln Leu Pro Asn Gly Tyr Tyr Tyr Glu Phe Ser Gly
835 840 845

Glu Ser Gln Tyr Leu Glu Glu Ala Phe Lys Thr Leu Gln Tyr Ile Val
850 855 860

Pro Val Ser Val Phe Ile Ile Phe Ile Leu Ile Val Phe Ala Leu Lys
865 870 875 880

Asn Leu Thr Asn Ser Leu Leu Cys Phe Phe Thr Leu Pro Phe Ala Phe
885 890 895

Leu Gly Gly Leu Ile Phe Met Asn Leu Met Gly Phe Asn Met Ser Val
900 905 910

Ala Ala Leu Val Gly Phe Leu Ala Leu Leu Gly Val Ala Ser Glu Thr
915 920 925

Ala Ile Val Met Ile Ile Tyr Leu Glu Asp Ala Phe Gln Lys Phe Ile
930 935 940

Lys Thr Pro Leu Lys Glu Gln Asn Ser Thr Thr Leu Lys Glu Ala Ile
945 950 955 960

Met His Gly Ala Val Leu Arg Val Arg Pro Lys Leu Met Thr Phe Phe
965 970 975

Ser Ile Leu Ala Ser Leu Ile Pro Ile Met Tyr Ser His Gly Thr Gly
980 985 990

Ser Glu Ile Met Lys Ser Ile Ala Ala Pro Met Leu Gly Gly Met Ile
995 1000 1005

Ser Ser Val Val Leu Thr Leu Phe Ile Ile Pro Thr Ala Tyr Phe
1010 1015 1020

Val Ile Lys Asn Ala Gly Ile Lys Ser Asn Gln Thr
1025 1030 1035

<210> 287

<211> 166

<212> PRT

<213> Helicobacter pylori

<400> 287

Met Ser Val Ser His Val Ala Leu Ile Leu Arg Lys Leu Phe Tyr His
1 5 10 15

Arg Gln Gly Val Phe Met Gly Gly Phe Ser Val Gly Met Leu Lys Asp
20 25 30

Tyr Val Asp Ile Phe Val Phe Ala Val Leu Gly Val Ala Ser Phe Leu
35 40 45

Ala Leu Trp Phe Ala Ile Glu Arg Val Ile Phe Tyr Ser Lys Val Asp
50 55 60

Leu Lys Ala Tyr Asp Asp Ile Asp Ala Leu Asn Leu Asp Leu Thr Lys
65 70 75 80

Asn Leu Thr Ile Leu Tyr Val Ile Phe Ser Asn Ala Pro Tyr Val Gly
85 90 95

Leu Leu Gly Thr Val Leu Gly Ile Met Val Ile Phe Tyr Asp Met Gly
100 105 110

Val Ser Gly Gly Met Asp Ala Lys Thr Ile Met Val Gly Leu Ser Leu
115 120 125

Ala Leu Lys Ala Thr Ala Leu Gly Leu Ala Val Ala Ile Pro Thr Leu
130 135 140

Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val Leu Ser Glu Lys
145 150 155 160

Phe Arg Ile Met Lys Lys
165

<210> 288

<211> 285

<212> PRT

<213> Helicobacter pylori

<400> 288

Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser
1   5   10   15

Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr
            20   25   30

Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr
        35   40   45

Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr
    50   55   60

Lys Thr Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys
65   70   75   80

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr
                85   90   95

Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro
            100   105   110

Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro
        115   120   125

Lys Val Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys
    130   135   140

Glu Glu Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val
145   150   155   160

Thr Thr Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn
                165   170   175

Lys Thr Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly
            180   185   190

Val Ser Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys
        195   200   205

Asn Arg Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val
    210   215   220

Leu Val Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys
225   230   235   240

Val Val Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu
                245   250   255

Ala Ile Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val
260 265 270

His Leu Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp
275 280 285

<210> 289

<211> 691

<212> PRT

<213> Helicobacter pylori

<400> 289

Met Lys Lys Ser Leu Leu Leu Ser Leu Ser Leu Ile Ala Ser Leu Ser
1 5 10 15

Arg Ala Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln Ile Gly
20 25 30

Glu Ala Val Gln Gln Val Lys Asn Thr Gly Ala Leu Gln Asn Leu Ala
35 40 45

Asp Arg Tyr Asp Asn Leu Asn Asn Leu Leu Asn Gln Tyr Asn Tyr Leu
50 55 60

Asn Ser Leu Val Asn Leu Ala Ser Thr Pro Ser Ala Ile Thr Gly Ala
65 70 75 80

Ile Asp Asn Leu Ser Ser Ser Ala Ile Asn Leu Thr Ser Ala Thr Thr
85 90 95

Thr Ser Pro Ala Tyr Gln Ala Val Ala Leu Ala Leu Asn Ala Ala Val
100 105 110

Gly Met Trp Gln Val Ile Ala Leu Phe Ile Gly Cys Gly Pro Gly Pro
115 120 125

Thr Asn Asn Gln Ser Tyr Gln Ser Phe Gly Asn Thr Pro Ala Leu Asn
130 135 140

Gly Thr Thr Thr Thr Cys Asn Gln Ala Tyr Gly Thr Gly Pro Asn Gly
145 150 155 160

Ile Leu Ser Ile Asp Glu Tyr Gln Lys Leu Asn Gln Ala Tyr Gln Ile
165 170 175

Ile Gln Thr Ala Leu Asn Gln Asn Gln Gly Gly Gly Met Pro Ala Leu
180 185 190

Asn Asp Thr Thr Lys Thr Gly Val Val Asn Ile Gln Gln Thr Asn Tyr
195 200 205

Arg Thr Thr Thr Gln Asn Asn Ile Ile Glu His Tyr Tyr Thr Glu Asn
210 215 220

Gly Lys Glu Ile Pro Val Ser Tyr Ser Gly Gly Ser Ser Phe Ser Pro
225 230 235 240

Thr Ile Gln Leu Thr Tyr His Asn Asn Ala Glu Asn Leu Leu Gln Gln
245 250 255

Ala Ala Thr Ile Met Gln Val Leu Ile Thr Gln Lys Pro His Val Gln
260 265 270

Thr Ser Asn Gly Gly Lys Ala Trp Gly Leu Ser Ser Thr Pro Gly Asn
275 280 285

Val Met Asp Ile Phe Gly Pro Ser Phe Asn Ala Ile Asn Glu Met Ile
290 295 300

Lys Asn Ala Gln Thr Ala Leu Ala Lys Thr Gln Gln Leu Asn Ala Asn
305 310 315 320

Glu Asn Ala Gln Ile Thr Gln Pro Asn Asn Phe Asn Pro Tyr Thr Ser
325 330 335

Lys Asp Lys Gly Phe Ala Gln Glu Met Leu Asn Arg Ala Glu Ala Gln
340 345 350

Ala Glu Ile Leu Asn Leu Ala Lys Gln Val Ala Asn Asn Phe His Ser
355 360 365

Ile Gln Gly Pro Ile Gln Gly Asp Leu Glu Glu Cys Lys Ala Gly Ser
370 375 380

Ala Gly Val Ile Thr Asn Asn Thr Trp Gly Ser Gly Cys Ala Phe Val
385 390 395 400

Lys Glu Thr Leu Asn Ser Leu Glu Gln His Thr Ala Tyr Tyr Gly Asn
405 410 415

Gln Val Asn Gln Asp Arg Ala Leu Ala Gln Thr Ile Leu Asn Phe Lys
420 425 430

Glu Ala Leu Asn Thr Leu Asn Lys Asp Ser Lys Ala Ile Asn Ser Gly
435 440 445

Ile Ser Asn Leu Pro Asn Ala Lys Ser Leu Gln Asn Met Thr His Ala
450 455 460

Thr Gln Asn Pro Asn Ser Pro Glu Gly Leu Leu Thr Tyr Ser Leu Asp
465 470 475 480

Ser Ser Lys Tyr Asn Gln Leu Gln Thr Ile Ala Gln Glu Leu Gly Lys
485 490 495

Asn Pro Phe Arg Arg Phe Gly Val Ile Asp Phe Gln Asn Asn Asn Gly
500 505 510

Ala Met Asn Gly Ile Gly Val Gln Val Gly Tyr Lys Gln Phe Phe Gly
515 520 525

Lys Lys Arg Asn Trp Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn
530 535 540

His Ala Tyr Ile Lys Ser Asn Phe Phe Asn Ser Ala Ser Asp Val Trp
545 550 555 560

Thr Tyr Gly Val Gly Met Asp Ala Leu Tyr Asn Phe Ile Asn Asp Lys
565 570 575

Asn Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val Gly Leu Phe
580 585 590

Gly Gly Phe Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser Gln Gln Val
595 600 605

Asn Leu Thr Met Met Asn Gly Ile Tyr Asn Ala Asn Val Ser Thr Ser
610 615 620

Asn Phe Gln Phe Leu Phe Asp Leu Gly Leu Arg Met Asn Leu Ala Arg
625 630 635 640

Pro Lys Lys Lys Asp Ser Asp His Ala Ala Gln His Gly Ile Glu Leu
645 650 655

Gly Phe Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser Phe Met Gly
660 665 670

Ala Lys Leu Glu Tyr Arg Arg Met Tyr Ser Leu Phe Leu Asn Tyr Val
675 680 685

Phe Ala Tyr
690

<210> 290

<211> 402

<212> PRT

<213> Helicobacter pylori

<400> 290

Met Leu Ala Lys Met Ser Phe Met Gln Asn Val Lys Asn Ile Gln Glu
1   5   10   15

Val Glu Val Ser His Lys Arg Val Leu Ile Arg Val Asp Phe Asn Val
            20   25   30

Pro Leu Asp Glu Asn Leu Asn Ile Thr Asp Asp Thr Arg Ile Arg Glu
        35   40   45

Ser Leu Pro Thr Ile Gln Tyr Cys Ile Asp Asn Lys Ala Lys Asp Ile
    50   55   60

Ile Leu Val Ser His Leu Gly Arg Pro Lys Gly Val Glu Glu Lys Leu
65   70   75   80

Ser Leu Lys Pro Phe Leu Lys Arg Leu Glu Arg Leu Leu Asn His Glu
                85   90   95

Val Val Phe Ser Gln Asn Ile Val Gln Leu Lys Gln Ala Leu Asn Glu
            100   105   110

Asn Ala Pro Thr Arg Ile Phe Leu Leu Glu Asn Ile Arg Phe Leu Arg
        115   120   125

Gly Glu Glu Glu Asn Asp Glu Asn Leu Ala Lys Asp Leu Ala Ser Leu
    130   135   140

Cys Asp Val Phe Val Asn Asp Ala Phe Gly Thr Ser His Arg Lys His
145   150   155   160

Ala Ser Thr Tyr Gly Thr Ala Lys Phe Ala Pro Ile Lys Val Ser Gly
                165   170   175

Phe Leu Leu Lys Lys Glu Ile Asp Ser Phe Tyr Gln Ala Phe Asn His
            180   185   190

Pro Leu Arg Pro Leu Leu Leu Ile Val Gly Gly Ala Lys Val Ser Ser
        195   200   205

Lys Leu Thr Leu Leu Lys Asn Ile Leu Asp Leu Ile Asp Lys Leu Ile
    210   215   220

Ile Ala Gly Ala Met Ser Asn Thr Phe Leu Lys Ala Leu Gly Tyr Asp
225   230   235   240

Val Gln Asp Ser Ser Val Glu Asp Ala Leu Ile Asn Asp Ala Leu Glu
                245   250   255

Leu Leu Gln Ser Ala Lys Glu Lys Lys Val Lys Val Tyr Leu Pro Ile
260 265 270

Asp Ala Val Thr Thr Asp Asp Ile Leu Asn Pro Lys His Ile Lys Ile
275 280 285

Ser Pro Val Gln Asp Ile Glu Pro Lys His Lys Ile Ala Asp Ile Gly
290 295 300

Pro Ala Ser Leu Lys Leu Phe Ser Glu Val Ile Glu Ser Ala Pro Thr
305 310 315 320

Ile Leu Trp Asn Gly Pro Leu Gly Val His Glu Lys Gln Glu Phe Ala
325 330 335

Arg Gly Thr Thr Phe Leu Ala His Lys Ile Ala Asp Thr Tyr Ala Phe
340 345 350

Ser Leu Ile Gly Gly Gly Asp Thr Ile Asp Ala Ile Asn Arg Ala Gly
355 360 365

Glu Lys Asp Asn Met Ser Phe Ile Ser Thr Gly Gly Gly Ala Ser Leu
370 375 380

Glu Leu Leu Glu Gly Lys Ile Leu Pro Cys Phe Glu Val Leu Asp Lys
385 390 395 400

Arg His

<210> 291

<211> 459

<212> PRT

<213> Helicobacter pylori

<400> 291

Val Val Leu Leu Thr Met Thr Lys Arg Leu Phe Lys Gly Leu Leu Ala
1 5 10 15

Val Ser Leu Ala Val Ser Leu His Gly Gly Glu Val Lys Glu Lys Lys
20 25 30

Pro Val Lys Pro Val Lys Glu Asp Pro Gln Glu Leu Ala Ala Lys Arg
35 40 45

Val Glu Ala Phe Ser Arg Phe Ser Asn Val Val Ser Glu Ile Glu Lys
50 55 60

Lys Tyr Val Asp Lys Ile Ser Ile Ser Glu Ile Met Thr Lys Ala Ile
65 70 75 80

Glu Gly Leu Leu Ser Asn Leu Asp Ala His Ser Ala Tyr Leu Asn Glu
85 90 95

Lys Lys Phe Lys Glu Phe Gln Ala Gln Thr Glu Gly Glu Phe Gly Gly
100 105 110

Leu Gly Ile Thr Val Gly Met Arg Asp Gly Val Leu Thr Val Ile Ala
115 120 125

Pro Leu Glu Gly Thr Pro Ala Tyr Lys Ala Gly Val Lys Ser Gly Asp
130 135 140

Asn Ile Leu Lys Ile Asn Asn Glu Ser Thr Leu Ser Met Ser Ile Asp
145 150 155 160

Asp Ala Ile Asn Leu Met Arg Gly Lys Pro Lys Thr Pro Ile Gln Ile
165 170 175

Thr Val Val Arg Lys Asn Glu Pro Lys Pro Leu Val Phe Asn Ile Ile
180 185 190

Arg Asp Ile Ile Lys Leu Pro Ser Val Tyr Val Lys Lys Ile Lys Glu
195 200 205

Thr Pro Tyr Leu Tyr Val Arg Val Ser Gly Phe Asp Lys Asn Val Thr
210 215 220

Lys Ser Val Leu Glu Gly Leu Lys Ala Asn Pro Lys Ala Lys Gly Ile
225 230 235 240

Val Leu Asp Leu Arg Gly Asn Pro Gly Gly Leu Leu Asn Gln Ala Val
245 250 255

Gly Leu Ser Asn Leu Phe Ile Lys Glu Gly Val Leu Val Ser Gln Lys
260 265 270

Gly Lys Asn Lys Glu Glu Asn Leu Glu Tyr Lys Ala Asn Gly Arg Ala
275 280 285

Pro Tyr Thr Asn Leu Pro Ile Ala Val Leu Val Asn Gly Gly Ser Ala
290 295 300

Ser Ala Ser Glu Ile Val Ala Gly Ala Leu Gln Asp His Lys Arg Ala
305 310 315 320

Val Ile Ile Gly Glu Lys Thr Phe Gly Lys Gly Ser Val Gln Met Leu
325 330 335

Leu Pro Val Asn Lys Asp Glu Ala Ile Lys Ile Thr Thr Ala Arg Tyr
340 345 350

Tyr Leu Pro Ser Gly Arg Thr Ile Gln Ala Lys Gly Ile Thr Pro Asp
355 360 365

Ile Val Ile Tyr Pro Gly Lys Val Pro Glu Asn Glu Asn Lys Phe Ser
370 375 380

Leu Lys Glu Ala Asp Leu Lys His His Leu Glu Gln Glu Leu Lys Lys
385 390 395 400

Ile Asp Asp Lys Thr Pro Asn Ser Lys Glu Ala Asp Lys Asp Lys Lys
405 410 415

Asn Glu Glu Glu Lys Glu Ile Thr Pro Lys Met Ile Asn Asp Asp Ile
420 425 430

Gln Leu Lys Thr Ala Ile Asp Ser Leu Lys Thr Trp Ser Ile Val Asp
435 440 445

Glu Lys Met Asp Glu Lys Ala Pro Lys Lys Lys
450 455

<210> 292

<211> 446

<212> PRT

<213> Helicobacter pylori

<400> 292

Met Asn Glu Thr Leu Tyr Cys Ser Phe Cys Lys Lys Pro Glu Ser Arg
1 5 10 15

Asp Pro Lys Lys Arg Arg Ile Ile Phe Ala Ser Asn Leu Asn Lys Asp
20 25 30

Val Cys Val Cys Glu Tyr Cys Ile Asp Val Met His Gly Glu Leu His
35 40 45

Lys Tyr Asp Asn Ser Leu Leu Ala Leu Lys Arg Asp Arg Leu Arg Arg
50 55 60

Met Glu Ser Ser Ala Tyr Glu Glu Glu Phe Leu Leu Ser Tyr Ile Pro
65 70 75 80

Ala Pro Lys Glu Leu Lys Ala Val Leu Asp Asn Tyr Val Ile Gly Gln
85 90 95

Glu Gln Ala Lys Lys Val Phe Ser Val Ala Val Tyr Asn His Tyr Lys
100 105 110

Arg Leu Ser Phe Lys Glu Lys Leu Lys Lys Gln Asp Asn Gln Asp Ser
115 120 125

Asn Val Glu Leu Glu His Leu Glu Glu Val Glu Leu Ser Lys Ser Asn
130 135 140

Ile Leu Leu Ile Gly Pro Thr Gly Ser Gly Lys Thr Leu Met Ala Gln
145 150 155 160

Thr Leu Ala Lys His Leu Asp Ile Pro Ile Ala Ile Ser Asp Ala Thr
165 170 175

Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu
180 185 190

Thr Arg Leu Leu Gln Ala Ser Asp Trp Asn Val Gln Lys Ala Gln Lys
195 200 205

Gly Ile Val Phe Ile Asp Glu Ile Asp Lys Ile Ser Arg Leu Ser Glu
210 215 220

Asn Arg Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala
225 230 235 240

Leu Leu Lys Ile Val Glu Gly Ser Leu Val Asn Ile Pro Pro Lys Gly
245 250 255

Gly Arg Lys His Pro Glu Gly Asn Phe Ile Gln Ile Asp Thr Ser Asp
260 265 270

Ile Leu Phe Ile Cys Ala Gly Ala Phe Asp Gly Leu Ala Glu Ile Ile
275 280 285

Lys Lys Arg Thr Thr Gln Asn Val Leu Gly Phe Thr Gln Glu Lys Met
290 295 300

Ser Lys Lys Glu Gln Glu Ala Ile Leu His Leu Val Gln Thr His Asp
305 310 315 320

Leu Val Thr Tyr Gly Leu Ile Pro Glu Leu Ile Gly Arg Leu Pro Val
325 330 335

Leu Ser Thr Leu Asp Ser Ile Ser Leu Glu Ala Met Val Asp Ile Leu
340 345 350

Gln Lys Pro Lys Asn Ala Leu Ile Lys Gln Tyr Gln Gln Leu Phe Lys
355 360 365

Met Asp Glu Val Asp Leu Ile Phe Glu Glu Glu Ala Ile Lys Glu Ile
370 375 380

Ala Gln Leu Ala Leu Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala
385 390 395 400

Ile Ile Glu Asp Phe Cys Leu Asp Ile Met Phe Asp Leu Pro Lys Leu
405 410 415

Lys Gly Ser Glu Val Arg Ile Thr Lys Asp Cys Val Leu Lys Gln Ala
420 425 430

Glu Pro Leu Ile Ile Ala Lys Thr His Ser Lys Ile Leu Pro
435 440 445

<210> 293

<211> 524

<212> PRT

<213> Helicobacter pylori

<400> 293

Met Arg Asp Phe Asn Asn Ala Gln Ile Thr Arg Leu Lys Val Arg Gln
1 5 10 15

Asn Ala Val Phe Glu Lys Leu Asp Leu Glu Phe Lys Asp Gly Leu Ser
20 25 30

Ala Ile Ser Gly Ala Ser Gly Val Gly Lys Ser Val Leu Ile Ala Ser
35 40 45

Leu Leu Gly Ala Phe Gly Leu Lys Glu Ser Asn Ala Ser Asn Ile Glu
50 55 60

Val Glu Leu Ile Ala Pro Phe Leu Asp Thr Glu Glu Tyr Gly Ile Phe
65 70 75 80

Arg Glu Asp Glu His Glu Pro Leu Val Ile Ser Val Ile Lys Lys Glu
85 90 95

Lys Thr Arg Tyr Phe Leu Asn Gln Thr Ser Leu Ser Lys Asn Thr Leu
100 105 110

Lys Ala Leu Leu Lys Gly Leu Ile Lys Arg Leu Ser Asn Asp Arg Phe
115 120 125

Ser Gln Asn Glu Leu Asn Asp Ile Leu Met Leu Ser Leu Leu Asp Gly
130 135 140

Tyr Ile Gln Asn Glu Asn Lys Ala Phe Ser Pro Leu Leu Gly Ala Leu
145 150 155 160

Glu Glu Lys Phe Thr Arg Leu Glu Lys Leu Glu Lys Glu Arg Arg Leu
165 170 175

Leu Glu Asp Lys Lys Arg Phe Gln Lys Asp Leu Glu Glu Arg Leu Asn
180 185 190

Phe Glu Lys Met Lys Leu Glu Arg Leu Asp Leu Lys Glu Asp Glu Tyr
195 200 205

Glu Arg Leu Leu Glu Gln Lys Lys Leu Leu Ser Ser Lys Glu Lys Leu
210 215 220

Asn Asp Lys Ile Ala Leu Ala Leu Glu Val Leu Glu Asn Thr His Lys
225 230 235 240

Ile Thr His Ala Leu Glu Ser Val Gly His Ser Ala Glu Phe Leu Lys
245 250 255

Ser Ala Leu Leu Glu Ala Ser Ala Leu Leu Glu Lys Glu Gln Ala Lys
260 265 270

Leu Glu Glu Cys Glu Arg Leu Asp Ile Glu Lys Val Leu Glu Arg Leu
275 280 285

Gly Met Leu Ser Gly Ile Ile Lys Asp Tyr Gly Ser Ile Met His Ala
290 295 300

Lys Glu Arg Leu Gly His Val Lys Asn Glu Leu His Asn Leu Lys Glu
305 310 315 320

Ile Asp Ser His Cys Glu Thr Tyr His Lys Glu Ile Glu Arg Leu Lys
325 330 335

Thr Glu Cys Leu Lys Leu Cys Glu Glu Ile Ser Gly Phe Arg Lys Glu
340 345 350

Tyr Leu Ala Gly Phe Asn Ala Leu Leu Ser Ala Lys Ala Lys Asp Leu
355 360 365

Leu Leu Lys Ser Pro Ser Leu Val Leu Glu Asp Ala Pro Met Ser Glu
370 375 380

Lys Gly Ala Gln Lys Leu Val Leu Asn Leu Gln Asn Ser Gln Leu Glu
385 390 395 400

Thr Leu Ser Ser Gly Glu Tyr Ser Arg Leu Arg Leu Ala Phe Met Leu
405 410 415

Leu Glu Met Glu Phe Leu Lys Asp Phe Lys Gly Val Leu Val Leu Asp
420 425 430

Glu Met Asp Ser Asn Leu Ser Gly Glu Glu Ser Leu Ala Val Ser Lys
435 440 445

Ala Leu Glu Thr Leu Ser Ser His Ser Gln Ile Phe Ala Ile Ser His
450 455 460

Gln Val His Ile Pro Ala Leu Ala Lys Asn His Ile Leu Val Phe Lys
465 470 475 480

Glu Asn His Lys Ser Leu Ala Lys Thr Leu Asn Asn Glu Glu Arg Val
485 490 495

Leu Glu Ile Ala Arg Met Ile Gly Gly Ser Glu Asn Ile Glu Ser Ala
500 505 510

Ile Ser Phe Ala Lys Glu Lys Leu Lys Ala Gln Glu
515 520

<210> 294

<211> 161

<212> PRT

<213> Helicobacter pylori

<400> 294

Met Pro Asp Glu Leu Arg Ala Glu Lys Ser Phe Pro Ser Lys Pro Tyr
1 5 10 15

Asp Ser Leu Lys Asn Lys Ser Glu Phe Asp Arg Val Tyr Gln Lys Gly
20 25 30

Phe Lys Lys His Asn Pro Phe Phe Ser Leu Phe Val Leu Asp Leu Ser
35 40 45

Gln Glu Pro Pro Lys Glu Lys Ala Gly Phe Lys Asp Pro Leu Phe Cys
50 55 60

Arg Leu Lys Asp Lys Lys Thr Leu Tyr Leu Leu Gly Leu Ser Val Ser
65 70 75 80

Lys Lys Val Gly Asn Ala Val Lys Arg Asn Leu Ile Lys Arg Arg Leu
85 90 95

Arg Ser Leu Thr Leu Lys His Ala Ala Leu Cys Gln Gly Leu Ala Leu
100 105 110

Val Phe Val Pro Arg Ser Asp Cys Tyr His Leu Asp Phe Trp Ala Leu
115 120 125

Glu Lys His Phe Leu Glu Met Leu Thr Ser Ile Lys Asn Tyr Met Asn
130 135 140

Lys Ala Leu Lys Asp Leu Lys Lys Gly Ile Thr His Thr Tyr Ala Lys
145 150 155 160

Gln

<210> 295

<211> 746

<212> PRT

<213> Helicobacter pylori

<400> 295

Met Leu Lys Leu Ala Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Ser
1 5 10 15

Phe Thr Ala Val Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe
20 25 30

Ile Glu Ala Gly Phe Glu Thr Gly Leu Leu Gln Gly Thr Gln Thr Lys
35 40 45

Glu Gln Thr Ile Ala Thr Thr Gln Glu Lys Pro Lys Pro Lys Pro Lys
50 55 60

Pro Lys Pro Ile Thr Pro Gln Ser Thr Tyr Gly Lys Tyr Tyr Ile Ser
65 70 75 80

Gln Ser Thr Val Leu Lys Asn Ala Thr Glu Leu Phe Ala Glu Asp Asn
85 90 95

Ile Thr Asn Leu Thr Phe Tyr Ser Leu Thr Pro Val Tyr Val Thr Ala
100 105 110

Tyr Asn Gln Glu Ser Ala Glu Glu Ala Gly Tyr Gly Asp Ser Ser Leu
115 120 125

Ile Met Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Ile Glu Leu
130 135 140

Ser Tyr Thr Asp Asn Gln Gly Asn Val Val Ser Leu Gly Val Ile Glu
145 150 155 160

Thr Ile Pro Lys Gln Ser Gln Ile Ile Leu Pro Ala Ser Leu Phe Asn
165 170 175

Asp Pro Gln Leu Asn Ala Asp Gly Phe Gln Gln Leu Gln Thr Ala Thr
180 185 190

Thr Arg Phe Ser Asp Ala Ser Thr Gln Asn Leu Phe Asp Lys Leu Ser
195 200 205

Lys Val Thr Thr Asn Leu Gln Met Thr Tyr Ile Asn Tyr Asn Gln Phe
210 215 220

Ser Ser Gly Asn Gly Ser Gly Ser Lys Pro Pro Cys Pro Pro Tyr Glu
225 230 235 240

Asn Gln Glu Asn Cys Thr Ala Lys Val Pro Pro Phe Thr Ser Gln Asp
245 250 255

Ala Lys Asn Leu Thr Asn Leu Met Leu Asn Met Met Ala Val Phe Asp
260 265 270

Ser Lys Ser Trp Glu Asp Ala Val Lys Asn Ala Pro Phe Gln Phe Ser
275 280 285

Asp Asn Asn Leu Ser Ala Pro Cys Tyr Ser Asn Tyr Ser Thr Cys Val
290 295 300

Asn Pro Tyr Asn Asp Gly Leu Val Asp Pro Lys Leu Ile Ala Lys Asn
305 310 315 320

Lys Gly Asp Glu Tyr Asn Ile Glu Asn Gly Gln Thr Gly Ser Val Ile
325 330 335

Leu Thr Pro Gln Asp Val Ile Tyr Ser Tyr Arg Val Thr Asn Asn Leu
340 345 350

Tyr Val Asn Leu Leu Pro Pro Arg Gly Gly Asp Leu Gly Leu Gly Ser
355 360 365

Gln Tyr Gly Gly Pro Asn Gly Pro Gly Asp Asp Gly Thr Asn Phe Gly
370 375 380

Ala Leu Gly Ile Leu Ser Pro Phe Leu Asp Pro Glu Ile Leu Phe Gly
385 390 395 400

Lys Glu Leu Asn Lys Val Ala Ile Met Gln Leu Arg Asp Ile Ile His
405 410 415

Glu Tyr Gly His Thr Leu Gly Tyr Thr His Asn Gly Asn Met Thr Tyr
420 425 430

Gln Arg Val Arg Met Cys Glu Glu Asn Asn Gly Pro Glu Glu Arg Cys
435 440 445

Lys Gly Gly Lys Ile Glu Gln Val Asp Gly Gln Glu Val Gln Val Phe
450 455 460

Asp Asn Gly His Glu Val Arg Asp Thr Asp Gly Ser Phe Tyr Asp Val
465 470 475 480

Cys Ser Arg Phe Gly Gly Gln Asn Gln Pro Ala Phe Pro Ser Ser Tyr
485 490 495

Pro Asn Ser Ile Tyr Thr Asp Cys Ser Gln Val Pro Ala Gly Leu Ile
500 505 510

Gly Val Thr Ser Ala Val Trp Gln Gln Leu Ile Asp Gln Asn Ala Leu
515 520 525

Pro Val Asp Tyr Thr Asn Leu Ser Ser Gln Thr Asn Tyr Leu Asn Ala
530 535 540

Ser Leu Asn Thr Gln Asp Phe Ala Thr Thr Met Leu Ser Ala Ile Ser
545 550 555 560

Gln Ser Leu Ser Ser Thr Arg Ser Ser Ala Thr Thr Tyr Arg Thr Ser
565 570 575

Lys Thr Ser Arg Pro Phe Gly Ala Pro Leu Leu Gly Val Asn Leu Lys
580 585 590

Met Gly Tyr Gln Lys Tyr Phe Asn Asp Tyr Leu Gly Leu Ser Ser Tyr
595 600 605

Gly Ile Ile Lys Tyr Asn Tyr Ala Gln Ala Asn Asn Glu Lys Ile Gln
610 615 620

Gln Leu Ser Tyr Gly Val Gly Met Asp Val Leu Phe Asp Phe Ile Thr
625 630 635 640

Asn Tyr Thr Asn Glu Lys Asn Pro Lys Asn Asn Leu Thr Lys Lys Val
645 650 655

Phe Thr Ser Ser Leu Gly Val Phe Gly Gly Leu Arg Gly Leu Tyr Asn
660 665 670

Ser Tyr Tyr Leu Leu Asn Gln Tyr Lys Gly Ser Gly Asn Leu Asn Val
675 680 685

Thr Gly Gly Leu Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser Val Gly
690 695 700

Ile Ser Val Pro Leu Val Gln Leu Lys Ser Arg Val Val Ser Ser Asp
705 710 715 720

Gly Ala Thr Thr Asn Ser Ile Thr Leu Asn Glu Gly Gly Ser His Phe
725 730 735

Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe
740 745

<210> 296

<211> 303

<212> PRT

<213> Helicobacter pylori

<400> 296

Met Lys Lys Ile Ile Leu Ala Cys Leu Met Ala Phe Val Gly Ala Asn
1 5 10 15

Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn
20 25 30

Thr Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu
35 40 45

Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val
50 55 60

Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys
65 70 75 80

Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu
85 90 95

Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Val Gln Lys Gly Ile
100 105 110

Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu Gln Gly Leu
115 120 125

Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr Leu Met Pro
130 135 140

Lys Val Cys Lys Gly Val Phe Leu Gln Gln Ser Lys Ser Met Gly Asp
145 150 155 160

Leu Leu Ala Lys Ala Met Pro Ile Glu Arg Ile Leu Lys Ala Tyr Ser
165 170 175

Val Pro Val Gly Ser Leu Glu Asn Tyr Glu Lys Ile Tyr Tyr Gln Asn
180 185 190

Ala Phe Lys Pro Lys Val Gln Ile Thr Phe Asp Asn Asn Gly Asp Ala
195 200 205

Glu Ile Lys Ser Ala Leu Ile Ser Ala Tyr Ala Arg Val Leu Thr Pro
210 215 220

Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val Phe Thr Asp
225 230 235 240

Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Val Val Ser Ala Ser Asp
245 250 255

Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val Asp Glu Lys
260 265 270

Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu Tyr Lys Glu
275 280 285

Leu Lys Asp Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr Gly Leu
290 295 300

<210> 297

<211> 1211

<212> PRT

<213> Helicobacter pylori

<400> 297

Met Lys Glu Asn Lys Ala Phe Thr His Leu His Leu His Thr Glu Tyr
1 5 10 15

Ser Leu Leu Asp Gly Ala Asn Lys Ile Lys Ile Leu Ala Lys Arg Val
20 25 30

Lys Glu Leu Gly Met Lys Ser Val Ser Val Thr Asp His Gly Asn Met
35 40 45

Phe Gly Ala Ile Asp Phe Tyr Thr Ser Met Lys Lys Glu Gly Ile Lys
50 55 60

Pro Ile Ile Gly Met Glu Ala Tyr Ile His Asn Asp Asp Asn Leu Ser
65 70 75 80

Ser Lys Glu Thr Lys Gln Arg Phe His Leu Cys Leu Phe Ala Lys Asn
85 90 95

Gln Glu Gly Tyr Glu Asn Leu Met Phe Leu Ser Ser Met Ala Tyr Leu
100 105 110

Glu Gly Phe Tyr Tyr Phe Pro Arg Ile Asn Lys Lys Leu Leu Lys Glu
115 120 125

His Ser Lys Gly Ile Ile Ala Ser Ser Ala Cys Leu Gln Gly Glu Val
130 135 140

Asn Tyr His Leu Asn Thr Asn Asn Glu Arg Asn Arg Lys Tyr Gly Ala
145 150 155 160

Lys Gly Tyr Asp Glu Ala Lys Lys Ile Ala Cys Glu Tyr Gln Glu Ile
165 170 175

Phe Glu Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp
180 185 190

Gln Arg Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly
195 200 205

Leu Lys Ile Ile Ala Thr Asn Asp Thr His Tyr Thr Met Pro Asn Asp
210 215 220

Ala Lys Ala Gln Glu Val Ala Met Cys Val Ala Met Gly Lys Thr Leu
225 230 235 240

Asn Asp Lys Gly Arg Leu Lys His Ser Val His Glu Phe Tyr Ile Lys
245 250 255

Ser Pro Glu Glu Met Ala Lys Leu Phe Ala Asp Ile Pro Glu Ala Leu
260 265 270

Glu Asn Thr Gln Glu Ile Ala Asp Lys Cys Val Leu Glu Ile Asp Leu
275 280 285

Lys Asp Asp Lys Lys Asn Pro Pro Thr Pro Pro Ser Phe Lys Phe Thr
290 295 300

Lys Ala Tyr Ala Gln Asn Glu Gly Leu Asn Phe Glu Asp Asp Ala Ser
305 310 315 320

Tyr Phe Ala Tyr Lys Ala Arg Glu Gly Leu Lys Glu Arg Leu Val Leu
325 330 335

Val Pro Lys Glu Lys His Asp Gln Tyr Lys Glu Arg Leu Glu Lys Glu
340 345 350

Ile Glu Val Ile Thr Asn Met Lys Phe Pro Gly Tyr Met Leu Ile Val
355 360 365

Trp Asp Phe Ile Arg Tyr Ala Lys Glu Met Gly Ile Pro Val Gly Pro
370 375 380

Gly Arg Gly Ser Ala Ala Gly Ser Leu Val Ala Phe Ala Leu Lys Ile
385 390 395 400

Thr Asp Ile Asp Pro Leu Lys Tyr Asp Leu Leu Phe Glu Arg Phe Leu
405 410 415

Asn Pro Glu Arg Ile Ser Met Pro Asp Ile Asp Thr Asp Phe Cys Gln
420 425 430

Arg Arg Arg Lys Glu Ile Ile Glu Tyr Met Ile Glu Lys Tyr Gly Lys
435 440 445

Tyr Asn Val Ala Gln Val Ile Thr Phe Asn Lys Met Leu Ala Lys Gly
450 455 460

Val Ile Arg Asp Val Ala Arg Val Leu Asp Met Pro Tyr Lys Glu Ala
465 470 475 480

Asp Asp Phe Ala Lys Leu Ile Pro Asn Arg Leu Gly Ile Thr Leu Lys
485 490 495

Gly Tyr Glu Lys Asn Gly Glu Phe Ile Glu Gly Ala Trp Glu Leu Glu
500 505 510

Pro Lys Ile Lys Glu Leu Val Glu Ser Asn Glu Leu Ala Lys Gln Val
515 520 525

Trp Glu Tyr Ser Leu Asn Leu Glu Asn Leu Asn Arg Asn Ala Gly Val
530 535 540

His Ala Ala Ala Leu Val Val Asp Ser Gln Lys Glu Leu Trp His Lys
545 550 555 560

Thr Pro Leu Phe Ala Ser Glu Lys Thr Gly Gly Ile Val Thr Gln Tyr
565 570 575

Ser Met Lys Tyr Leu Glu Pro Val Asp Leu Ile Lys Phe Asp Phe Leu
580 585 590

Gly Leu Lys Thr Leu Thr Val Ile Asp Asp Ala Leu Lys Ile Ile Lys
595 600 605

Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser Leu Asp Met Asp Asp
610 615 620

Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp Thr Val Gly Ile Phe
625 630 635 640

Gln Ile Glu Ser Gly Met Phe Gln Gly Leu Asn Lys Arg Leu Arg Pro
645 650 655

Ser Ser Phe Glu Asp Ile Ile Ala Ile Ile Ala Leu Gly Arg Pro Gly
660 665 670

Pro Met Glu Ser Gly Met Val Asp Asp Phe Val Asn Arg Lys His Gly
675 680 685

Val Glu Pro Ile Ala Tyr Ala Phe Lys Glu Leu Glu Pro Ile Leu Lys
690 695 700

Pro Thr Tyr Gly Thr Ile Val Tyr Gln Glu Gln Val Met Gln Ile Val
705 710 715 720

Gln Thr Ile Gly Gly Phe Ser Leu Gly Glu Ala Asp Leu Ile Arg Arg
725 730 735

Ala Met Gly Lys Lys Asp Ala Gln Ile Met Ala Asp Asn Lys Ala Lys
740 745 750

Phe Val Glu Gly Ala Lys Asn Leu Gly His Asp Gly Gln Lys Ala Ala
755 760 765

Asn Leu Trp Asp Leu Ile Val Lys Phe Ala Gly Tyr Gly Phe Asn Lys
770 775 780

Ser His Ser Ala Ala Tyr Ala Met Ile Thr Phe Gln Thr Ala Tyr Leu
785 790 795 800

Lys Thr Tyr Tyr Lys His Glu Phe Met Ala Ala Met Leu Thr Ser Glu
805 810 815

Ser Asn Lys Ile Glu Ser Val Ala Arg Tyr Ile Asp Glu Val Arg Ala
820 825 830

Leu Glu Ile Glu Val Met Pro Pro His Ile Asn Ser Ser Met Gln Asp
835 840 845

Phe Ser Val Ala Glu Phe Lys Asn Gln Lys Gly Glu Leu Glu Lys Lys
850 855 860

Ile Val Phe Gly Leu Gly Ala Ile Lys Gly Val Gly Gly Glu Pro Ile
865 870 875 880

Lys Asn Ile Ile Glu Glu Arg Ala Lys Gly Asp Tyr Lys Ser Leu Glu
885 890 895

Asp Phe Ile Ser Arg Val Asp Phe Ser Lys Leu Thr Lys Lys Ser Leu
900 905 910

Glu Pro Leu Val Lys Ser Gly Ser Leu Asp Asn Leu Gly Tyr Thr Arg
915 920 925

Lys Thr Met Leu Ala Asn Leu Asp Leu Ile Cys Asp Ala Gly Arg Ala
930 935 940

Lys Asp Lys Ala Asn Glu Met Met Gln Gly Gly Asn Ser Leu Phe Gly
945 950 955 960

Ala Met Glu Gly Gly Thr Lys Glu Gln Val Val Leu Asp Met Ile Asp
965 970 975

Leu Gly Glu His Asp Ala Lys Thr Leu Leu Glu Cys Glu Tyr Glu Thr
980 985 990

Leu Gly Ile His Val Ser Gly Asn Pro Leu Asp Glu Phe Lys Glu Glu
995 1000 1005

Ile Lys Gly Phe Lys Asn Leu Val Lys Ser Ile Asp Ile Glu Glu
1010 1015 1020

Leu Glu Ile Gly Ser Gln Ala Tyr Leu Leu Gly Lys Ile Met Glu
1025 1030 1035

Val Lys Lys Lys Ile Gly Lys Arg Ser Gly Lys Pro Tyr Gly Ile
1040 1045 1050

Ala Asp Ile Leu Asp Arg Tyr Gly Lys Phe Glu Leu Met Leu Phe
1055 1060 1065

Glu Lys Gln Leu Asn Ala Leu Glu Glu Leu Asp Ile Asn Lys Pro
1070 1075 1080

Leu Val Phe Lys Cys Lys Ile Glu Glu Gln Glu Glu Val Val Arg
1085 1090 1095

Leu Arg Leu Phe Glu Ile Leu Asp Leu Glu Ser Ala Arg Glu Val
1100 1105 1110

Lys Ile Pro Lys Ala Arg Tyr Lys Asp Pro Glu Lys Gln Lys Glu
1115 1120 1125

Glu Val Arg Glu Ile Pro Pro Met Glu Met Leu Ala Ser Ser Ser
1130 1135 1140

Cys Ser Leu Ala Ile Val Leu Glu Asn Asp Val Lys Lys Glu Phe
1145 1150 1155

Leu Arg Gln Ile Lys Glu Ser Ala Leu Lys His Gln Gly Lys Arg
1160 1165 1170

Pro Leu Tyr Leu Ile Ile Lys Asp Lys Asp Lys Gln Phe Lys Ile
1175 1180 1185

Gln Ser Asp Leu Met Val Asn Glu Lys Ile Lys Asp Asp Phe Lys
1190 1195 1200

Gly Leu Glu Trp Arg Asp Leu Ala
1205 1210

<210> 298

<211> 186

<212> PRT

<213> Helicobacter pylori

<400> 298

Met Thr Leu Leu Val Gly Leu Gly Asn Pro Thr Leu Arg Tyr Ala His
1 5 10 15

Thr Arg His Asn Ala Gly Phe Asp Ile Leu Asp Ser Leu Val Ser Glu
20 25 30

Leu Asp Leu Ser Phe Thr Phe Ser Pro Lys His Asn Ala Phe Leu Cys
35 40 45

Val Tyr Lys Asp Phe Ile Phe Leu Lys Pro Gln Thr Tyr Met Asn Leu
50 55 60

Ser Gly Glu Ser Val Leu Ser Ala Lys Asn Phe Tyr Lys Thr Lys Glu
65 70 75 80

Leu Leu Ile Val His Asp Asp Leu Asp Leu Pro Leu Gly Val Val Arg
85 90 95

Phe Lys Asn Gly Gly Gly Asn Gly Gly His Asn Gly Leu Lys Ser Ile
100 105 110

Asp Leu Leu Cys Ser Asn Ser Tyr Tyr Arg Leu Arg Val Gly Ile Ser
115 120 125

Lys Gly Ile Gly Val Ile Glu His Val Leu Ser Lys Phe His Lys Asn
130 135 140

Glu Glu Pro Leu Lys Asn Ala Ala Phe Glu His Ala Lys Asn Ala Leu
145 150 155 160

Lys Phe Phe Ile Glu Ser His Asp Phe Asn Ala Met Gln Asn Arg Phe
165 170 175

Thr Leu Lys Lys Pro Leu Lys Ile Glu Ser
180 185

<210> 299

<211> 479

<212> PRT

<213> Helicobacter pylori

<400> 299

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro
1 5 10 15

Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser Pro
20 25 30

His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Lys Pro Arg
35 40 45

Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr Leu
50 55 60

Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp Glu
65 70 75 80

Lys Leu Ser Leu Glu Thr Thr Leu Asn Pro Asn Arg Pro Thr Ile Pro
85 90 95

Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Ser His
100 105 110

Pro His Gln Met Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln Asn
115 120 125

Lys Pro His Ser Ser Gln Gln Pro Ser Gln Asn Phe Ser Tyr Pro Glu
130 135 140

Pro Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro Leu
145 150 155 160

Ala Ile Pro Ser Lys Ile Ser Pro Thr Asn Glu Thr Gln Thr Pro Thr
165 170 175

Asn Asp Thr Lys Pro Pro Leu Lys His Ser Ser Glu Asp Gln Glu Ser
180 185 190

Asn Leu Phe Ile Thr Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn Thr
195 200 205

Ser Asn Ala Asp Ile Ser Glu Asn Asn Glu Ser Asn Glu Asn Lys Asp
210 215 220

Asn Val Glu Lys Gln Ala Ile Arg Asp Ala Asn Ile Lys Glu Phe Ala
225 230 235 240

Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg Pro
245 250 255

Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp Ile
260 265 270

Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile Ile
275 280 285

Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu Glu
290 295 300

Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala Arg
305 310 315 320

Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly Thr
325 330 335

Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu
340 345 350

Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg
355 360 365

Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu
370 375 380

Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu Leu
385 390 395 400

Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His
405 410 415

Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val
420 425 430

Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu Ile
435 440 445

Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn Ser
450 455 460

Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
465 470 475

<210> 300

<211> 271

<212> PRT

<213> Helicobacter pylori

<400> 300

Met Asn Ala Phe Lys Arg Ile Ile Ser Val Gly Val Ile Ala Leu Gly
1 5 10 15

Leu Phe Asn Leu Leu Asp Ala Lys His His Lys Glu Lys Lys Glu Asn
20 25 30

His Lys Ile Thr Arg Glu Leu Lys Val Gly Ala Asn Pro Val Pro His
35 40 45

Ala Gln Ile Leu Gln Ser Val Val Asp Asp Leu Lys Glu Lys Gly Ile
50 55 60

Lys Leu Val Ile Val Ser Phe Thr Asp Tyr Val Leu Pro Asn Leu Ala
65 70 75 80

Leu Asn Asp Gly Ser Leu Asp Ala Asn Tyr Phe Gln His Arg Pro Tyr
85 90 95

Leu Asp Arg Phe Asn Leu Asp Arg Lys Met His Leu Val Gly Leu Ala
100 105 110

Asn Ile His Val Glu Pro Leu Arg Phe Tyr Ser Gln Lys Ile Thr Asp
115 120 125

Ile Lys Asn Leu Lys Lys Gly Ser Val Ile Ala Val Pro Asn Asp Pro
130 135 140

Ala Asn Gln Gly Arg Ala Leu Ile Leu Leu His Lys Gln Gly Leu Ile
145 150 155 160

Ala Leu Lys Asp Pro Ser Asn Leu Tyr Ala Thr Glu Phe Asp Ile Val
165 170 175

Lys Asn Pro Tyr Asn Ile Lys Ile Lys Pro Leu Glu Ala Ala Leu Leu
180 185 190

Pro Lys Val Leu Gly Asp Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr
195 200 205

Ala Leu Gln Ala Lys Leu Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp
210 215 220

Ser Pro Tyr Ala Asn Leu Ile Ala Ala Arg Glu Asp Asn Ala Gln Asp
225 230 235 240

Glu Ala Ile Lys Thr Leu Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg
245 250 255

Lys Phe Ile Leu Asp Thr Tyr Lys Gly Ala Ile Ile Pro Ala Phe
260 265 270

<210> 301

<211> 588

<212> PRT

<213> Helicobacter pylori

<400> 301

Met Lys Asn Leu Arg Tyr Lys Leu Leu Leu Phe Val Phe Ile Gly Phe
1 5 10 15

Trp Gly Leu Leu Ala Leu Asn Leu Phe Ile Leu Ser Val Lys Asn Gln
20 25 30

Glu Tyr Tyr Glu Lys Leu Ala Glu Arg Asn Met Thr Lys Lys Glu Phe
35 40 45

Leu Val Pro Thr Arg Gly Asn Ile Thr Asp Arg Asn Asp Glu Phe Leu
50 55 60

Ala Thr Asn Glu Leu Val Phe Gly Val Phe Leu Pro Ser Gly Leu Lys
65 70 75 80

Gln Lys Asp Leu Leu Glu Lys Ile Glu Ile Ile Gln Lys Phe Phe Pro
85 90 95

Asn Phe Ser Lys Glu Thr Leu Leu Asn Asn Tyr Gln Lys Glu Asn Ser
100 105 110

Leu Tyr Asn His Asn Leu Ile Lys Val Val Gly Phe Ile Pro Tyr Ala
115 120 125

Thr Met Gln Pro Leu Tyr Ala Lys Leu Ile Gln Thr Gln Gly Ile Phe
130 135 140

Ala Leu Pro Leu Asp Lys Arg Tyr Tyr Pro Asn Asn Ala Leu Ala Ser
145 150 155 160

His Val Leu Gly Tyr Val Gly Val Ala Ser Leu Gln Asp Leu Lys Asp
165 170 175

Asp Glu Glu Asn Gln Tyr Ser Gln Ile Val Gly Lys Thr Gly Ile Glu
180 185 190

Lys Glu Tyr Asn Lys Leu Leu Gln Gly Lys Val Gly Tyr Lys Ile Met
195 200 205

Arg Val Asn Ala Leu Asn Gln Glu Leu Ala Thr Leu Glu Val Val Leu
210 215 220

Pro Ser Thr Asn Asn His Leu Gln Leu Ser Leu Asp Lys Arg Leu Gln
225 230 235 240

Lys Glu Ala Asp Lys Leu Phe Glu Asn Lys Arg Gly Ala Ile Leu Val
245 250 255

Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly Ser Tyr Pro Glu
260 265 270

Tyr Asn Leu Asn Asp Phe Val Gly Gly Ile Ser Gln Asp Lys Trp Gln
275 280 285

Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu Asn Arg Phe Ala Asn
290 295 300

Ala Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser
305 310 315 320

Phe Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro
325 330 335

Pro Phe Ile Glu Val Gly Lys His Lys Phe Arg Asp Trp Lys Lys Thr
340 345 350

Gly His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp
355 360 365

Val Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Lys Leu Ser
370 375 380

Lys Thr Leu Arg Glu Val Gly Phe Gly Glu Lys Thr Gly Val Asp Leu
385 390 395 400

Pro Asn Glu Phe Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys
405 410 415

Arg Phe Asn Gln Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile
420 425 430

Gly Gln Gly Ser Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr
435 440 445

Gly Leu Ile Ala Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile Asn
450 455 460

Asn Lys Gln Pro Leu Lys Asp Pro Leu Asn Ser Phe Gln Lys Lys Lys
465 470 475 480

Leu Gln Ala Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp
485 490 495

Gly Thr Ala Tyr His Ser Thr Arg Gly Ser Lys Ile Thr Leu Ala Cys
500 505 510

Lys Thr Gly Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn
515 520 525

Arg Met Lys Glu Lys Asp Met Glu Tyr Phe His Arg Ser His Ala Trp
530 535 540

Ile Thr Ala Phe Leu Pro Tyr Glu Lys Pro Lys Tyr Ala Ile Thr Ile
545 550 555 560

Leu Val Glu His Gly Glu Gly Gly Ser Lys Leu Gly Gly Leu Leu Val
565 570 575

Lys Met Ser Asn Lys Leu Tyr Glu Leu Gly Tyr Leu
580 585

<210> 302

<211> 206

<212> PRT

<213> Helicobacter pylori

<400> 302

Met Phe Ser Gly Leu Ile His Gln Ile Ala Lys Val Lys Ser Phe His
1 5 10 15

Asn Asn Ile Leu Asn Ile Glu Ser Asp Leu Asn Pro Lys Leu Gly Asp
20 25 30

Ser Ile Ala Ile Asn Gly Ala Cys Leu Thr Ala Ile Glu Ser Ser Lys
35 40 45

Thr His Phe Ser Val Glu Leu Ser Gln Lys Thr Gln Asn Ser Val Ala
50 55 60

Leu Glu Asn Tyr Lys Asp Leu Val His Ile Glu Pro Ala Leu Lys Ala
65 70 75 80

Asp Ala Ser Leu Asp Gly His Phe Val Gln Gly His Ile Asp Ala Ile
85 90 95

Gly Val Ile Glu Lys Ile Ile His Asn Ala Asn Gln Val Asp Phe Phe
100 105 110

Ile Ser Ala Ser Glu Glu Thr Leu Leu Leu Cys Val Glu Gln Gly Ser
115 120 125

Ile Ala Val Asp Gly Val Ser Leu Thr Leu Ser Lys Val Glu Glu Lys
130 135 140

Gly Phe Trp Leu Thr Ile Ile Pro Tyr Thr Leu Glu Asn Thr Leu Phe
145 150 155 160

Lys Ala Tyr Lys Leu Lys Arg Arg Val Asn Ile Glu Thr Asp Met Leu
165 170 175

Val Arg Ser Val Ala Ser Ile Leu Lys Lys Thr Lys Gly Phe Glu Lys
180 185 190

Asn Phe Ser Trp Asn Glu Ala Asp Ala Leu Thr Leu Gly Tyr
195 200 205

<210> 303

<211> 40

<212> PRT

<213> Helicobacter pylori

<400> 303

Lys Lys Ser Glu Arg Phe Lys Ile Glu Leu Lys Pro Phe Lys Lys Arg
1 5 10 15

Pro Asn Arg Gly Ala His Arg Arg Ala Leu Phe Gln Ala Tyr Arg Ser
20 25 30

Gly Phe Ala Phe Arg Arg Ser His
35 40

<210> 304

<211> 17

<212> PRT

<213> Helicobacter pylori

<400> 304

Trp Phe Ala Lys Lys Asp Phe Ser Ala Trp Ser Ala Thr Lys Arg Ala
1 5 10 15

Phe

<210> 305

<211> 68

<212> PRT

<213> Helicobacter pylori

<400> 305

Asn Leu Gln Thr His Leu Lys Arg Leu Lys Arg Ser Glu Phe Val Gly
1 5 10 15

Gln Lys Gly Ile Arg Gly His Gly Glu Val Phe Phe Lys Arg Asn Phe
20 25 30

Asn Ala Gln Pro Tyr Leu Ile Gly Phe Thr Gly Leu Asp Phe Trp Gln
35 40 45

Thr Phe Arg Leu Ala Cys Glu Cys Asp Gly Phe Asp Cys His Gly Phe
50 55 60

Asn Gly Val Leu
65

<210> 306

<211> 29

<212> PRT

<213> Helicobacter pylori

<400> 306

Thr Gln Ala Ile Ile Leu Lys Lys Asn Gln Ala Trp Gly Arg Gly Trp
1 5 10 15

Ile Met Arg Gly Val Ala Ser Ile Ile Asn Ser Arg Glu
20 25

<210> 307

<211> 48

<212> PRT

<213> Helicobacter pylori

<400> 307

Ala Met Trp Ile Leu Leu Lys Thr Ser Lys Thr Arg Asn Ser Lys Lys
1 5 10 15

Ile Val Trp Asn Leu Ser Lys Gly Leu Met Ser Gln Ser Pro Leu Ser
20 25 30

Leu Pro Leu Phe Ile Thr Leu Gly Ala Leu Ser Pro Leu Lys Lys Lys
35 40 45

<210> 308

<211> 23

<212> PRT

<213> Helicobacter pylori

<400> 308

Lys Lys Lys Lys Ser Lys Asn Ser Lys Asn Ser Pro Trp Ala Trp Lys
1 5 10 15

Cys Leu Ser Met Cys Gly Val
20

<210> 309

<211> 31

<212> PRT

<213> Helicobacter pylori

<400> 309

Lys Lys Leu Ile Lys Ser Leu Ala Leu Lys Lys Asp Thr Ala Ile Val
1 5 10 15

Met Lys Ser Thr Pro Asn Thr Ala Lys Ser Gly Lys Ile Arg Ala
20 25 30

<210> 310

<211> 24

<212> PRT

<213> Helicobacter pylori

<400> 310

Arg Gly Ala Thr Pro Pro Arg Lys Lys Thr Leu Phe Leu Lys Lys Pro
1   5   10   15

Ser Val Leu Ser Arg Pro Asn Ser
            20

<210> 311

<211> 18

<212> PRT

<213> Helicobacter pylori

<400> 311

Ser Ala Gln Pro Pro Ser Leu Lys Arg Ser Leu Gly Gly Leu Lys Ala
1   5   10   15

Met Ala

<210> 312

<211> 14

<212> PRT

<213> Helicobacter pylori

<400> 312

Lys His Asp His Gly Phe Trp Val Arg His Ser Arg Glu Phe
1   5   10

<210> 313

<211> 20

<212> PRT

<213> Helicobacter pylori

<400> 313

Ala Lys Asn Thr Ala Leu Lys Ser Leu Ala Leu Gly Ile Arg Ala Met
1   5   10   15

Ala Met Cys Met
            20

<210> 314

<211> 63

<212> PRT

<213> Helicobacter pylori

<400> 314

Arg Phe Glu Arg Gln Asn Leu Ser Leu Arg Tyr Gly Ser Ile Gly Leu
1 5 10 15

Gln Gln Leu Phe Ile His Arg Lys Pro His Tyr Gln Asn Lys Ser Asn
20 25 30

Gly Asn Leu Cys Gly Phe Asp Tyr His His Arg Leu Ile Arg Ala Ser
35 40 45

Gln Trp Val Leu Gln His Ser Lys Ser Ala Gln Gln Thr Gln Arg
50 55 60

<210> 315

<211> 49

<212> PRT

<213> Helicobacter pylori

<400> 315

Ser Ser Val Ser Ser Lys Lys Pro Ala Lys Asn Ser Leu Thr Arg Phe
1 5 10 15

Leu Ser Ser Gln Gly Ile Ile Leu Thr Gly Ala Met Asn Thr Leu Lys
20 25 30

Thr Ile Cys Ile Ser Leu Asn Pro Cys Arg Leu Phe Tyr Met Pro Leu
35 40 45

Leu

<210> 316

<211> 34

<212> PRT

<213> Helicobacter pylori

<400> 316

Lys Trp Asn Ile Ser Thr Pro Lys Pro Pro Pro Lys Asn Gly Ala Ile
1 5 10 15

Gly Trp Gly Ile Ile Ser Leu Leu Ser Lys Thr Ile Leu Ile Ile Leu
20 25 30

Gly Ile

<210> 317

<211> 27

<212> PRT

<213> Helicobacter pylori

<400> 317

Lys Thr Arg Trp Ile Pro Thr Glu Lys Trp Arg Asn Ser Thr Met Glu
1 5 10 15

Ala Ala Arg Arg Pro Phe Phe Arg Pro Phe Asn
20 25

<210> 318

<211> 76

<212> PRT

<213> Helicobacter pylori

<400> 318

Lys Asn Phe Arg Ala His Asp Phe Phe Glu Arg Arg Asp Cys Gln Tyr
1 5 10 15

Phe Tyr Ser Val Trp Arg Arg Ala Met Gly Asp Ser Ser Ser Tyr His
20 25 30

Ala Ser Gly Trp Ala Lys Leu Arg Gly Gly Ser Gly Ser Gly Phe Tyr
35 40 45

Gly Tyr Arg Leu Gly Arg Cys Leu Asp Glu Tyr Asp Thr Ala Phe Leu
50 55 60

Gly Phe Ala Arg Phe Ser His Cys Gly Phe Gly Arg
65 70 75

<210> 319

<211> 24

<212> PRT

<213> Helicobacter pylori

<400> 319

Lys Ala Arg Leu Lys Arg Phe Gln Ile Ile Pro Leu Ile Ser Ala Glu
1 5 10 15

Lys Ala Met Leu Gln Ala Met Arg
20

<210> 320

<211> 17

<212> PRT

<213> Helicobacter pylori

<400> 320

Arg Ala Pro Phe Arg Arg Glu Pro Trp Arg Leu Gly Gly Cys Cys Asn
1 5 10 15

Leu

<210> 321

<211> 23

<212> PRT

<213> Helicobacter pylori

<400> 321

Phe Thr Arg His Lys Gln Thr Ser Arg Ser Lys Arg Ser Lys Ser Leu
1 5 10 15

Ser Val Lys Asn Gly Val Arg
20

<210> 322

<211> 26

<212> PRT

<213> Helicobacter pylori

<400> 322

Phe Phe Ser Tyr Ile Gln Tyr Glu Arg Arg Ser Ser Gly Tyr His Arg
1 5 10 15

Ala Trp Pro Phe Phe Arg Glu Arg Phe Asp
20 25

<210> 323

<211> 21

<212> PRT

<213> Helicobacter pylori

<400> 323

Arg Asp Leu Leu Ala Ile Pro Gln Arg Phe Ala Arg Lys Gln Ala Phe
1 5 10 15

Lys Lys Pro Ser Leu
20

<210> 324

<211> 11

<212> PRT

<213> Helicobacter pylori

<400> 324

Lys Ser Pro Lys Lys Ala Thr Lys Lys Arg Phe
1 5 10

<210> 325

<211> 13

<212> PRT

<213> Helicobacter pylori

<400> 325

Ala Leu Glu Gln Arg Asp Glu Arg Phe Thr Arg Gly Gly
1 5 10

<210> 326

<211> 101

<212> PRT

<213> Helicobacter pylori

<400> 326

Pro Ile Ser Cys Lys Ala Pro Lys Phe Val Val Ser Leu Cys Asn Ser
1   5   10   15

Gly Met Pro Leu Asp Leu Gly Pro Trp Lys Gly Lys Thr Ala Thr Lys
            20   25   30

Ser Leu Ser Asn Ser Leu Phe Leu Lys Arg Ser Lys Asn Ser Leu Trp
        35   40   45

Val Leu Lys Thr Ile Ala Leu Ala Leu Thr Phe Leu Cys Ser Ser Leu
    50   55   60

Met Ala Glu Ile Leu Ile Thr Ala Leu Pro Lys Leu Pro Phe Lys Ile
65   70   75   80

Leu Ser Pro Pro Leu Ala Ala Lys Gly Ser Leu Thr Gly Arg Lys Ile
                85   90   95

Ser Val Phe Arg Leu
            100

<210> 327

<211> 15

<212> PRT

<213> Helicobacter pylori

<400> 327

Lys Ser Ile Thr Ser Arg Gln Ala Ile Lys Pro Ile Leu Arg Ala
1   5   10   15

<210> 328

<211> 38

<212> PRT

<213> Helicobacter pylori

<400> 328

Phe Lys Thr Leu Val Glu Leu Phe Lys Ser Gln Ile Pro Gly Ala Phe
1   5   10   15

Arg Lys His Ser His Pro Arg His Ser Asn Phe Ser Val Phe Lys Lys
            20   25   30

Ser Gly Lys Ser Gly Val
        35

<210> 329

<211> 31

<212> PRT

<213> Helicobacter pylori

<400> 329

Asn Ala Ile Met Lys Pro Lys Lys Pro Gln Tyr Leu Lys Asn Ser Leu
1 5 10 15

Asn Ser Ser Asn Phe Met Ile Thr Pro Leu Leu Lys Ser Lys Pro
20 25 30

<210> 330

<211> 16

<212> PRT

<213> Helicobacter pylori

<400> 330

Ile Lys Ala Leu Lys Pro Ser Leu Phe Glu Arg Leu Asn Ser Leu Asn
1 5 10 15

<210> 331

<211> 62

<212> PRT

<213> Helicobacter pylori

<400> 331

Ala Met Leu Phe Phe Arg Phe Val Thr Val Ser Pro Thr Tyr Ala Gln
1 5 10 15

Pro Ala Pro Gln Val Leu Glu Val Thr Val Pro Asp Gly Val Pro Arg
20 25 30

Arg Leu Pro Ser Leu Pro Phe Ser Trp His Thr Pro Lys Glu Ser Phe
35 40 45

Thr Asn Ala Ala Gly Ile Leu Ser Lys Ser Phe Thr Thr Ala
50 55 60

<210> 332

<211> 35

<212> PRT

<213> Helicobacter pylori

<400> 332

Gly Leu Phe Gln Asn Leu Thr Pro His Ser Lys Thr Pro Arg Ser Leu
1   5   10   15

Arg Arg Ala Asn Ala Leu Lys Gln Lys Arg Val Leu Thr Pro His Leu
            20   25   30

Leu Ala Cys
        35

<210> 333

<211> 37

<212> PRT

<213> Helicobacter pylori

<400> 333

Phe Val Gly Pro Gln Glu Val Pro Pro Ile Ala Thr Pro Lys Lys Asn
1   5   10   15

Pro Lys Cys Lys Phe Ser Arg Leu Lys Ile Ala Gly Leu Asn Asn Thr
            20   25   30

Ser Val Pro Ala Pro
        35

<210> 334

<211> 97

<212> PRT

<213> Helicobacter pylori

<400> 334

Ile Arg Ala Phe Phe Lys Gly Val Asn Leu Ala Asn Phe Ile Asp Tyr
1   5   10   15

Gly Arg Asp Ser Arg Ile Phe Gly Ser Asp Asp Phe Ile Ser Gly Val
            20   25   30

Ser Gly Ser Gly Glu Phe Ala Cys Lys Lys Thr Pro Val Phe Gly Tyr
        35   40   45

Phe Ala Ile Asp Leu Lys Ile Pro Phe Ala Asn Gly Cys Leu Val Val
50 55 60

Leu Ser Ile Gln Pro Phe Lys Arg Pro Ser His Gln Ile Ala Val Arg
65 70 75 80

Lys Thr Pro Val Phe Lys Arg Val Gln Phe Ala Gly Ile Lys Thr Arg
85 90 95

Leu

<210> 335

<211> 41

<212> PRT

<213> Helicobacter pylori

<400> 335

Lys Phe Phe Ser Asn His Leu Arg Arg Lys Val Val Phe Ile Asp Ile
1 5 10 15

Ser Leu His Val Asn Ala Phe Leu Ala His Ser Asn Lys Ser His Ser
20 25 30

Met Gln Gln Ser Val Lys Ala Ile Phe
35 40

<210> 336

<211> 14

<212> PRT

<213> Helicobacter pylori

<400> 336

Ser Val Gly Val Lys Lys Ser Pro Pro Asn Ser Thr Ser Ala
1 5 10

<210> 337

<211> 66

<212> PRT

<213> Helicobacter pylori

<400> 337

Thr Leu Thr Cys Lys Lys Val Ala Ser Lys Arg Ala Leu Ile Cys Ala
1   5   10   15

Leu Ile Ser Leu Thr Leu Asn Thr Ser Thr Ser Ser Pro Phe Tyr Ser
            20   25   30

Lys Arg Val Arg Ser Leu Lys Ser Pro Lys Asn Met Ile Lys Thr Lys
        35   40   45

Asn Pro Thr Pro Ala Ser His Asn Ala Phe Cys Met Gly Val Gly Lys
    50   55   60

Val Ile
65

<210> 338

<211> 63

<212> PRT

<213> Helicobacter pylori

<400> 338

Ala Ser Met Ser Leu Ser Asn Pro Val Pro Leu Gly Ile Ala Ala Val
1   5   10   15

Thr Pro Thr Ile Phe Ser Ser Phe Leu Ala Asn Ser Lys Arg Val Leu
            20   25   30

Glu Tyr Ala Ser Val Gly Asp Lys Ile Ala Leu Leu Asp Phe Leu Asp
        35   40   45

Lys Pro Val Ser Lys Ser Lys Gly Pro Thr Pro Cys His Phe Ser
    50   55   60

<210> 339

<211> 85

<212> PRT

<213> Helicobacter pylori

<400> 339

Ile Phe Leu Ser Asn Thr Ser Leu Cys Met Gly Arg Thr Asn Cys Asn
1   5   10   15

Thr Lys Ser Asn Glu Asn Ala Leu Ala Ser Leu Asn Ser Thr Ser Lys
            20   25   30

Lys Ser Met His Ser Lys Arg Ala Leu Leu Lys Ser Phe Asn Phe Ser
35 40 45

Cys Ala Phe Leu Ser Met Gly Met Glu Leu Ser Ile Pro Thr Ser Ser
50 55 60

Ile Ser Cys Trp Ile Cys Arg Leu Ser Ala Ile Lys Lys Phe Pro Val
65 70 75 80

Glu Gln Pro Lys Ser
85

<210> 340

<211> 83

<212> PRT

<213> Helicobacter pylori

<400> 340

Arg Asp Phe Gln Val Leu Lys His Arg Leu His Pro Phe Phe Phe Ile
1 5 10 15

Phe Thr Gln Gln Ala Met Ile His Lys Asn Ser Asp Gln Ile Ile Leu
20 25 30

Asn Gly Ser Val Gln Gln Arg Ser Asp His Arg Arg Ile His Ala Pro
35 40 45

Thr His Arg Ala Gln Asn Leu Ser Val Ser Asp Phe Phe Phe Gln Ser
50 55 60

Cys Asp Phe Ser Leu Ser Glu Met Leu His Pro Pro Ser Phe Phe Thr
65 70 75 80

Ala Ala Asn

<210> 341

<211> 39

<212> PRT

<213> Helicobacter pylori

<400> 341

Ile Ile His Met Arg Gly Asp His Ser His His Met Pro Ser Phe Phe
1 5 10 15

Gln Arg Phe Lys Lys Thr Lys Arg Cys His Arg Ser Ala Ile Thr Gly
20 25 30

Val Phe Lys Thr Ile His Asp
35

<210> 342

<211> 44

<212> PRT

<213> Helicobacter pylori

<400> 342

Ile Ile Ile Pro Ala Val Leu Ala Asn Asp His Ala His Ile Asn Leu
1 5 10 15

Arg Leu Gly Val Asp Lys Lys Arg Ala Ser Phe Leu Asp Ile Glu Lys
20 25 30

Gly Lys Ser Gly Arg Phe Ala Ile Phe His Ala Asp
35 40

<210> 343

<211> 25

<212> PRT

<213> Helicobacter pylori

<400> 343

Lys Asn Arg Pro Ser Lys Asn Pro Leu Ala Gln Asn Ala Val Val Ser
1 5 10 15

Ala Leu Ala Pro Gly Lys Thr Ser Tyr
20 25

<210> 344

<211> 22

<212> PRT

<213> Helicobacter pylori

<400> 344

Lys Pro Ser Ser Val Trp Ile Tyr Lys Pro Ile Ile Arg Gly Lys Asn
1 5 10 15

Ile Gln Thr Ile Pro Ser
20

<210> 345

<211> 49

<212> PRT

<213> Helicobacter pylori

<400> 345

Ser Ser Val Ser Ser Lys Lys Pro Ala Lys Asn Ser Leu Thr Arg Phe
1 5 10 15

Leu Ser Ser Gln Gly Ile Ile Leu Thr Gly Ala Met Asn Thr Leu Lys
20 25 30

Thr Ile Cys Ile Ser Leu Asn Pro Cys Arg Leu Phe Tyr Met Pro Leu
35 40 45

Leu

<210> 346

<211> 43

<212> PRT

<213> Helicobacter pylori

<400> 346

Arg Ala Arg Ser Arg Ser Leu Leu Gly Phe Phe Leu Leu Lys Ala Ser
1 5 10 15

Cys Lys Thr Pro His Lys Ser Leu Asn Phe His Leu Ser Asn Ser Lys
20 25 30

Gln Gly Lys Trp Arg Ile Lys Ser Phe Trp Lys
35 40

<210> 347

<211> 87

<212> PRT

<213> Helicobacter pylori

<400> 347

Val Ser Glu Ile Leu Ser Thr Leu Val Ser Pro Ser Lys Leu Pro Glu
1 5 10 15

Glu Pro Lys Ala Lys Leu Met Arg Trp Gly Ala Ser Ala Pro Phe Leu
20 25 30

Gly Ser Asn Cys Lys Arg Gly Gly Phe Met Pro Ala Ser Asp Pro Ser
35 40 45

Leu Leu Lys Cys Lys Arg Pro Pro Ser Asn Thr Leu Gly Leu Ala Ala
50 55 60

Asp Pro Pro Thr Asn Ser Pro Gly Ser Gly Thr Ile Thr Leu Lys Phe
65 70 75 80

His Ser Ala Pro Pro Leu Leu
85

<210> 348

<211> 36

<212> PRT

<213> Helicobacter pylori

<400> 348

Leu Pro Asn Leu Asn Lys Ile Ser Ser Ser Ser Phe Thr Lys Tyr Thr
1 5 10 15

Ser Lys Thr Ser Gly Leu Met Trp His Ser Leu Lys Gly Phe His Phe
20 25 30

Pro Phe Lys Ala
35

<210> 349

<211> 26

<212> PRT

<213> Helicobacter pylori

<400> 349

Ser Arg Phe Arg Glu Arg Val Ala Ala Leu Phe Thr Lys Arg Ala Gln
1 5 10 15

Arg Lys Arg Phe Arg His Ser Phe Ile Ala
20 25

<210> 350

<211> 41

<212> PRT

<213> Helicobacter pylori

<400> 350

Asn Ile His Trp Pro His Ala Pro Asn Arg Ser Leu Leu Asn Pro Lys
1 5 10 15

Ile Val Ala Gly Asn Pro Ser Ser Leu Glu Tyr Arg Phe Ala Leu Asn
20 25 30

Ser Pro Gln Lys Ala Pro Gln His Arg
35 40

<210> 351

<211> 101

<212> PRT

<213> Helicobacter pylori

<400> 351

Pro Ile Ser Cys Lys Ala Pro Lys Phe Val Val Ser Leu Cys Asn Ser
1 5 10 15

Gly Met Pro Leu Asp Leu Gly Pro Trp Lys Gly Lys Thr Ala Thr Lys
20 25 30

Ser Leu Ser Asn Ser Leu Phe Leu Lys Arg Ser Lys Asn Ser Leu Trp
35 40 45

Val Leu Lys Thr Ile Ala Leu Ala Leu Thr Phe Leu Cys Ser Ser Leu
50 55 60

Met Ala Glu Ile Leu Ile Thr Ala Leu Pro Lys Leu Pro Phe Lys Ile
65 70 75 80

Leu Ser Pro Pro Leu Ala Ala Lys Gly Ser Leu Thr Gly Arg Lys Ile
85 90 95

Ser Val Phe Arg Leu
100

<210> 352

<211> 27

<212> PRT

<213> Helicobacter pylori

<400> 352

Glu Ser Leu Val Leu Lys Pro Ile Leu Gly Lys Arg Arg Cys Lys Gly
1 5 10 15

Cys Cys Pro Pro Ser Lys Pro Leu Leu Ala Leu
20 25

<210> 353

<211> 28

<212> PRT

<213> Helicobacter pylori

<400> 353

Gly Ser Asn Glu Arg Ser His Lys Glu Arg Leu Ser Ile Gln Thr His
1 5 10 15

Arg Ile Ala Ser Arg Asp Phe Asp Ile Cys Pro Leu
20 25

<210> 354

<211> 92

<212> PRT

<213> Helicobacter pylori

<400> 354

Leu Gly Gly Asn Lys Ser Phe Thr Leu Tyr Ser His His Thr Ser Gln
1 5 10 15

Pro Phe Phe Ser Lys Arg Leu Ala Thr Cys Ser Lys Thr Ser Leu Ser
20 25 30

Lys Gln Gly Leu Phe Val Arg Leu Ser Met Lys Lys Ala Ser Gly Thr
35 40 45

Pro His Phe Leu Cys Arg Leu Lys His Gln Ser Gly Arg Phe Ser Ile
50 55 60

Met Val Phe Arg Arg Phe Phe Pro Leu Leu Gly Thr Asn Ser Thr Phe
65 70 75 80

Ser Ile Ala Ser Lys Ala Thr Ser Leu Lys Val Phe
85 90

<210> 355

<211> 33

<212> PRT

<213> Helicobacter pylori

<400> 355

Ala Phe Val Leu Lys Pro Cys Lys Lys Ala Cys Ser Trp Ser Phe Lys
1 5 10 15

Phe Ser Leu Ala Asn Ser Thr Leu Glu Ser Lys Leu Leu Tyr Ser Phe
20 25 30

Lys

<210> 356

<211> 62

<212> PRT

<213> Helicobacter pylori

<400> 356

Glu Ser Ile Ser Ser Leu Ile Leu Ser Lys Ile Met Ile Val Ser Leu
1 5 10 15

Met Glu Tyr Pro Ile Lys Val Ser Lys Ala Ala Ile Thr Ser Lys Phe
20 25 30

Ile Ser Ile Leu Lys Thr Ile Thr Glu Leu Ala Thr Lys Ile Thr Ser
35 40 45

Cys Thr Ser Ala Met Thr Leu Ala Lys Ala Lys Arg His Ser
50 55 60

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